

## TITLE OF THE INVENTION

### CONE SNAIL PEPTIDES

#### CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] The present application is related to and claims priority under 35 USC §119(e) to U.S. provisional patent application Serial No. 60/267,408 filed 9 February 2001, incorporated herein by reference.

[0002] This invention was made with Government support under Grant No. PO1 GM48677 awarded by the National Institute of General Medical Sciences, National Institutes of Health, Bethesda, Maryland. The United States Government has certain rights in the invention.

#### BACKGROUND OF THE INVENTION

[0003] The present invention is directed to conotoxin peptides, derivatives or pharmaceutically acceptable salts thereof. The present invention is further directed to the use of this peptide, derivatives thereof and pharmaceutically acceptable salts thereof for the treatment of disorders associated with voltage-gated ion channels, ligand-gated ion channels and/or receptors. The invention is further directed to nucleic acid sequences encoding the conotoxin peptides and encoding propeptides, as well as the propeptides.

[0004] The publications and other materials used herein to illuminate the background of the invention, and in particular, cases to provide additional details respecting the practice, are incorporated by reference, and for convenience are referenced in the following text by author and date and are listed alphabetically by author in the appended bibliography.

[0005] *Conus* is a genus of predatory marine gastropods (snails) which envenomate their prey. Venomous cone snails use a highly developed projectile apparatus to deliver their cocktail of toxic conotoxins into their prey. In fish-eating species such as *Conus magus* the cone detects the presence of the fish using chemosensors in its siphon and when close enough extends its proboscis and fires a hollow harpoon-like tooth containing venom into the fish. This immobilizes the fish and enables the cone snail to wind it into its mouth via an attached filament.

For general information on *Conus* and their venom see the website address <http://grimwade.biochem.unimelb.edu.au/cone/referenc.html>. Prey capture is accomplished through a sophisticated arsenal of peptides which target specific ion channel and receptor subtypes. Each *Conus* species venom appears to contain a unique set of 50-200 peptides. The

composition of the venom differs greatly between species and between individual snails within each species, each optimally evolved to paralyse its prey. The active components of the venom are small peptide toxins, typically 12-30 amino acid residues in length and are typically highly constrained peptides due to their high density of disulphide bonds.

[0006] The venoms consist of a large number of different peptide components that when separated exhibit a range of biological activities: when injected into mice they elicit a range of physiological responses from shaking to depression. The paralytic components of the venom that have been the focus of recent investigation are the  $\alpha$ -,  $\omega$ - and  $\mu$ -conotoxins. All of these conotoxins act by preventing neuronal communication, but each targets a different aspect of the process to achieve this. The  $\alpha$ -conotoxins target nicotinic ligand gated channels, the  $\mu$ -conotoxins target the voltage-gated sodium channels and the  $\omega$ -conotoxins target the voltage-gated calcium channels (Olivera et al., 1985; Olivera et al., 1990). For example a linkage has been established between  $\alpha$ -,  $\alpha A$ - &  $\phi$ -conotoxins and the nicotinic ligand-gated ion channel;  $\omega$ -conotoxins and the voltage-gated calcium channel;  $\mu$ -conotoxins and the voltage-gated sodium channel;  $\delta$ -conotoxins and the voltage-gated sodium channel;  $\kappa$ -conotoxins and the voltage-gated potassium channel; conantokins and the ligand-gated glutamate (NMDA) channel.

[0007] However, the structure and function of only a small minority of these peptides have been determined to date. For peptides where function has been determined, three classes of targets have been elucidated: voltage-gated ion channels; ligand-gated ion channels, and G-protein-linked receptors.

[0008] *Conus* peptides which target voltage-gated ion channels include those that delay the inactivation of sodium channels, as well as blockers specific for sodium channels, calcium channels and potassium channels. Peptides that target ligand-gated ion channels include antagonists of NMDA and serotonin receptors, as well as competitive and noncompetitive nicotinic receptor antagonists. Peptides which act on G-protein receptors include neurotensin and vasopressin receptor agonists. The unprecedented pharmaceutical selectivity of conotoxins is at least in part defined by a specific disulfide bond frameworks combined with hypervariable amino acids within disulfide loops (for a review see McIntosh et al., 1998).

[0009] There are drugs used in the treatment of pain, which are known in the literature and to the skilled artisan. See, for example, Merck Manual, 16th Ed. (1992). However, there is a demand for more active analgesic agents with diminished side effects and toxicity and which are non-addictive. The ideal analgesic would reduce the awareness of pain, produce analgesia over a

wide range of pain types, act satisfactorily whether given orally or parenterally, produce minimal or no side effects, be free from tendency to produce tolerance and drug dependence.

[0010] Due to the high potency and exquisite selectivity of the conopeptides, several are in various stages of clinical development for treatment of human disorders. For example, two *Conus* peptides are being developed for the treatment of pain. The most advanced is  $\omega$ -conotoxin MVIIA (ziconotide), an N-type calcium channel blocker (see Heading, C., 1999; U.S. Patent No. 5,859,186).  $\omega$ -Conotoxin MVIIA, isolated from *Conus magus*, is approximately 1000 times more potent than morphine, yet does not produce the tolerance or addictive properties of opiates.  $\omega$ -Conotoxin MVIIA has completed Phase III (final stages) of human clinical trials and has been approved as a therapeutic agent.  $\omega$ -Conotoxin MVIIA is introduced into human patients by means of an implantable, programmable pump with a catheter threaded into the intrathecal space. Preclinical testing for use in post-surgical pain is being carried out on another *Conus* peptide, conulakin-G, isolated from *Conus geographus* (Craig et al. 1999). Conulakin-G is a 16 amino acid O-linked glycopeptide whose C-terminus resembles neurotensin. It is an agonist of neurotensin receptors, but appears significantly more potent than neurotensin in inhibiting pain in *in vivo* assays.

[0011] In view of a large number of biologically active substances in *Conus* species it is desirable to further characterize them and to identify peptides capable of treating disorders voltage-gated ion channels, ligand-gated ion channels and/or receptors. Surprisingly, and in accordance with this invention, Applicants have discovered novel conotoxins that can be useful for the treatment of disorders involving voltage-gated ion channels, ligand-gated ion channels and/or receptors and could address a long felt need for a safe and effective treatment.

#### SUMMARY OF THE INVENTION

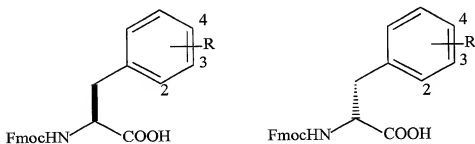
[0012] The present invention is directed to conotoxin peptides, derivatives or pharmaceutically acceptable salts thereof. The present invention is further directed to the use of this peptide, derivatives thereof and pharmaceutically acceptable salts thereof for the treatment of disorders associated with voltage-gated ion channels, ligand-gated ion channels and/or receptors. The invention is further directed to nucleic acid sequences encoding the conotoxin peptides and encoding propeptides, as well as the propeptides.

[0013] More specifically, the present invention is directed to conotoxin peptides, having the amino acid sequences set forth in Tables 1-14 below.

[0014] The present invention is also directed to derivatives or pharmaceutically acceptable salts of the conotoxin peptides or the derivatives. Examples of derivatives include peptides in which the Arg residues may be substituted by Lys, ornithine, homoarginine, nor-Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys or any synthetic basic amino acid; the Lys residues may be substituted by Arg, ornithine, homoarginine, nor-Lys, or any synthetic basic amino acid; the Tyr residues may be substituted with meta-Tyr, ortho-Tyr, nor-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr, nitro-Tyr or any synthetic hydroxy containing amino acid; the Ser residues may be substituted with Thr or any synthetic hydroxylated amino acid; the Thr residues may be substituted with Ser or any synthetic hydroxylated amino acid; the Phe residues may be substituted with any synthetic aromatic amino acid; the Trp residues may be substituted with Trp (D), neo-Trp, halo-Trp (D or L) or any aromatic synthetic amino acid; and the Asn, Ser, Thr or Hyp residues may be glycosylated. The halogen may be iodo, chloro, fluoro or bromo; preferably iodo for halogen substituted-Tyr and bromo for halogen-substituted Trp. The Tyr residues may also be substituted with the 3-hydroxyl or 2-hydroxyl isomers (meta-Tyr or ortho-Tyr, respectively) and corresponding O-sulpho- and O-phospho-derivatives. The acidic amino acid residues may be substituted with any synthetic acidic amino acid, e.g., tetrazolyl derivatives of Gly and Ala. The aliphatic amino acids may be substituted by synthetic derivatives bearing non-natural aliphatic branched or linear side chains  $C_nH_{2n+2}$  up to and including  $n=8$ . The Leu residues may be substituted with Leu (D). The Glu residues may be substituted with Glu. The Gla residues may be substituted with Glu. The N-terminal Gln residues may be substituted with pyroGlu. The Met residues may be substituted with norleucine (Nle). The Cys residues may be in D or L configuration and may optionally be substituted with homocysteine (D or L).

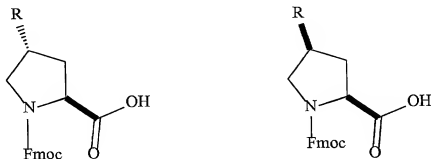
[0015] Examples of synthetic aromatic amino acid include, but are not limited to, nitro-Phe, 4-substituted-Phe wherein the substituent is  $C_1-C_3$  alkyl, carboxyl, hydroxymethyl, sulphomethyl, halo, phenyl, -CHO, -CN, -SO<sub>3</sub>H and -NHAc. Examples of synthetic hydroxy containing amino acid, include, but are not limited to, such as 4-hydroxymethyl-Phe, 4-hydroxyphenyl-Gly, 2,6-dimethyl-Tyr and 5-amino-Tyr. Examples of synthetic basic amino acids include, but are not limited to, N-1-(2-pyrazoliny)-Arg, 2-(4-piperiny)-Gly, 2-(4-piperiny)-Ala, 2-[3-(2S)pyrrolininy]-Gly and 2-[3-(2S)pyrrolininy]-Ala. These and other synthetic basic amino acids, synthetic hydroxy containing amino acids or synthetic aromatic amino acids are described in Building Block Index, Version 3.0 (1999 Catalog, pages 4-47 for

hydroxy containing amino acids and aromatic amino acids and pages 66-87 for basic amino acids; see also <http://www.amino-acids.com>), incorporated herein by reference, by and available from RSP Amino Acid Analogues, Inc., Worcester, MA. The residues containing protecting groups are deprotected using conventional techniques. Examples of synthetic acid amino acids include those derivatives bearing acidic functionality, including carboxyl, phosphate, sulfonate and synthetic tetrazolyl derivatives such as described by Ornstein et al. (1993) and in U.S. Patent No. 5,331,001, each incorporated herein by reference, and such as shown in the following schemes 1-3.



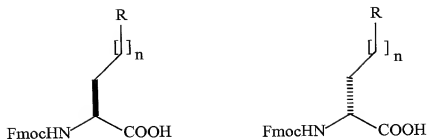
R=COOH, tetrazole,  $\text{CH}_2\text{COOH}$ , 4- $\text{NHSO}_2\text{CH}_3$ , 4- $\text{NHSO}_2\text{Phenyl}$ , 4- $\text{CH}_2\text{SO}_3\text{H}$ ,  $\text{SO}_3\text{H}$ , 4- $\text{CH}_2\text{PO}_3\text{H}_2$ ,  $\text{CH}_2\text{CH}_2\text{COOH}$ ,  $\text{OCH}_2\text{Tetrazole}$ ,  $\text{CH}_2\text{STetrazole}$ ,  $\text{HNTetrazole}$ ,  $\text{CONHSO}_2\text{R}_1$  where  $\text{R}_1$  is  $\text{CH}_3$  or  $\text{Phenyl}$   $\text{SO}_2^-\text{Tetrazole}$ ,  $\text{CH}_2\text{CH}_2\text{SO}_3\text{H}$ , 1,2,4-tetrazole, 3-isoxazolone, amidotetrazole,  $\text{CH}_2\text{CH}_2\text{PO}_3\text{H}_2$

Scheme 1



R = COOH, tetrazole,  $\text{CH}_2\text{COOH}$ ,  $\text{CH}_2\text{tetrazole}$

Scheme 2



R = COOH, tetrazole,  $\text{CH}_2\text{COOH}$ ,  $4\text{-NHSO}_2\text{CH}_3$ ,  $4\text{-NHSO}_2\text{Phenyl}$ ,  
 $4\text{-CH}_2\text{SO}_3\text{H}$ ,  $\text{SO}_3\text{H}$ ,  $4\text{-CH}_2\text{PO}_3\text{H}_2$ ,  $\text{CH}_2\text{CH}_2\text{COOH}$ ,  $\text{OCH}_2\text{Tetrazole}$ ,  
 $\text{CH}_2\text{STetrazole}$ ,  $\text{HNTetrazole}$ ,  $\text{CONHSO}_2\text{R}_1$  where  $\text{R}_1$  is  $\text{CH}_3$  or Phenyl  
 $\text{SO}_2\text{-Tetrazole}$ ,  $\text{CH}_2\text{CH}_2\text{SO}_3\text{H}$ , 1,2,4-tetrazole, 3-isoxazolone,  
 amidotetrazole,  $\text{CH}_2\text{CH}_2\text{PO}_3\text{H}_2$  n = 0, 1, 2, or 3

Scheme 3

[0016] Optionally, in the conotoxin peptides of the present invention, the Asn residues may be modified to contain an N-glycan and the Ser, Thr and Hyp residues may be modified to contain an O-glycan (e.g., g-N, g-S, g-T and g-Hyp). In accordance with the present invention, a glycan shall mean any N-, S- or O-linked mono-, di-, tri-, poly- or oligosaccharide that can be attached to any hydroxy, amino or thiol group of natural or modified amino acids by synthetic or enzymatic methodologies known in the art. The monosaccharides making up the glycan can include D-allose, D-altrose, D-glucose, D-mannose, D-gulose, D-idose, D-galactose, D-talose, D-galactosamine, D-glucosamine, D-N-acetyl-glucosamine (GlcNAc), D-N-acetyl-galactosamine (GalNAc), D-fucose or D-arabinose. These saccharides may be structurally modified, e.g., with one or more O-sulfate, O-phosphate, O-acetyl or acidic groups, such as sialic acid, including combinations thereof. The glycan may also include similar polyhydroxy groups, such as D-penicillamine 2,5 and halogenated derivatives thereof or polypropylene glycol derivatives. The glycosidic linkage is beta and 1-4 or 1-3, preferably 1-3. The linkage between the glycan and the amino acid may be alpha or beta, preferably alpha and is 1-.

[0017] Core O-glycans have been described by Van de Steen et al. (1998), incorporated herein by reference. Mucin type O-linked oligosaccharides are attached to Ser or Thr (or other hydroxylated residues of the present peptides) by a GalNAc residue. The monosaccharide building blocks and the linkage attached to this first GalNAc residue define the "core glycans," of which eight have been identified. The type of glycosidic linkage (orientation and

connectivities) are defined for each core glycan. Suitable glycans and glycan analogs are described further in U.S. Serial No. 09/420,797 filed 19 October 1999 and in PCT Application No. PCT/US99/24380 filed 19 October 1999 (PCT Published Application No. WO 00/23092), each incorporated herein by reference. A preferred glycan is Gal( $\beta$ 1 $\rightarrow$ 3)GalNAc( $\alpha$ 1 $\rightarrow$ ).

5 [0018] Optionally, in the conotoxin peptides described above, pairs of Cys residues may be replaced pairwise with isoteric lactam or ester-thioether replacements, such as Ser/(Glu or Asp), Lys/(Glu or Asp), Cys/(Glu or Asp) or Cys/Ala combinations. Sequential coupling by known methods (Barnay et al., 2000; Hraby et al., 1994; Bitan et al., 1997) allows replacement of native Cys bridges with lactam bridges. Thioether analogs may be readily synthesized using halo-Ala residues commercially available from RSP Amino Acid Analogues. In addition, individual Cys residues may be replaced with homoCys, seleno-Cys or penicillamine, so that disulfide bridges may be formed between Cys-homoCys or Cys-penicillamine, or homoCys-penicillamine and the like.

[0019] The present invention is further directed to derivatives of the above peptides and peptide derivatives which are acyclic permutations in which the cyclic permutants retain the native bridging pattern of native toxin. See, Craik et al. (2001).

10 [0020] The present invention is further directed to a method of treating disorders associated with voltage-gated ion channels, ligand-gated ion channels and/or receptor disorders in a subject comprising administering to the subject an effective amount of the pharmaceutical composition comprising a therapeutically effective amount of a conotoxin peptide described herein or a pharmaceutically acceptable salt or solvate thereof. The present invention is also directed to a pharmaceutical composition comprising a therapeutically effective amount of a conotoxin peptide described herein or a pharmaceutically acceptable salt or solvate thereof and a pharmaceutically acceptable carrier.

15 [0021] More specifically, the present invention is also directed to nucleic acids which encode conotoxin peptides of the present invention or which encodes precursor peptides for these conotoxin peptides, as well as the precursor peptide. The nucleic acid sequences encoding the precursor peptides of other conotoxin peptides of the present invention are set forth in Table 1. Table 1 also sets forth the amino acid sequences of these precursor peptides.

20 [0022] Another embodiment of the invention contemplates a method of identifying compounds that mimic the therapeutic activity of the instant peptide, comprising the steps of: (a) conducting a biological assay on a test compound to determine the therapeutic activity; and (b)

comparing the results obtained from the biological assay of the test compound to the results obtained from the biological assay of the peptide. The peptide is labeled with any conventional label, preferably a radioiodine on an available Tyr. Thus, the invention is also directed to radioiodinated conotoxins.

#### DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENT

[0023] The present invention is directed to conotoxin peptides, derivatives or pharmaceutically acceptable salts thereof. The present invention is further directed to the use of this peptide, derivatives thereof and pharmaceutically acceptable salts thereof for the treatment of disorders associated with voltage-gated ion channels, ligand-gated ion channels and/or receptors. The invention is further directed to nucleic acid sequences encoding the conotoxin peptides and encoding propeptides, as well as the propeptides.

[0024] The present invention, in another aspect, relates to a pharmaceutical composition comprising an effective amount of a conotoxin peptides, a mutein thereof, an analog thereof, an active fragment thereof or pharmaceutically acceptable salts or solvates. Such a pharmaceutical composition has the capability of acting at voltage-gated ion channels, ligand-gated ion channels and/or receptors, and are thus useful for treating a disorder or disease of a living animal body, including a human, which disorder or disease is responsive to the partial or complete blockade of such channels or receptors comprising the step of administering to such a living animal body, including a human, in need thereof a therapeutically effective amount of a pharmaceutical composition of the present invention.

[0025] Examples of voltage-gated ion channels include the voltage-gated calcium channel, the voltage-gated sodium channel, the voltage-gated potassium channel and the proton-gated ion channel. Examples of ligand-gated channels include the nicotinic ligand-gated ion channel, ligand-gated glutamate (NMDA) channel and the ligand-gated 5HT<sub>3</sub> (serotonin) channel. Examples of receptors include the G-protein receptors. Activity of  $\psi$ -conotoxins is described in U.S. Patent No. 5,969,096 and in Shon et al. (1997). Activity of bromosleeper conotoxins is described in U.S. Patent No. 5,889,147 and in Craig et al. (1997). Activity of  $\sigma$ -conotoxins is described in U.S. Patent No. 5,889,147. Activity of contryphan conotoxins is described in U.S. Patent No. 6,077,934 and in Jimenez et al. (1996). Activity of conopressins is described in Cruz et al. (1987) and in Kruszynski et al. (1990). Activity of  $\gamma$ -conotoxins is described in Fainzilber et al. (1998). Activity of  $\alpha$ A-conotoxins (kappaA??) is described in

Jacobsen et al. (1997) and in Hopkins et al. (1995). Activity of  $\alpha$ -conotoxins is described in U.S. Patent Nos. 4,447,356 and 5,514,774. Activity of  $\tau$ -conotoxins is described in U.S. Serial No. 09/497,491 (PCT/US00/03021, PCT published application WO 00/46371) as an antagonist for acetylcholine receptors and as analgesic agents for the treatment of pain (whether acute or chronic), including migraine, chronic pain, and neuropathic pain, without undesirable side effects. Activity of conotulakins is described in U.S. Serial No. 09/420,797 (PCT/US99/24380, PCT published application WO 00/23092). Each of these references is incorporated herein by reference.

[0026] Since  $\sigma$ -conotoxins are antagonists of the 5HT<sub>3</sub> receptor, they are also useful in treating irritable bowel syndrome (IBS) and visceral pain. Visceral pain is a common experience in health and disease. Chronic visceral hyperalgesia in the absence of detectable organic disease has been implicated in many common functional bowel disorders (FDB), such as IBS, non-ulcer dyspepsia (NUD) and non-cardiac chest pain (NCCP).

[0027] Pain in IBS cannot be explained by normal perception of abnormal motility. In the majority of patients, sensory perception itself is abnormal. Most visceral afferent information is part of the reflex activity of digestion and does not reach conscious perception. Increasing evidence suggests that long term changes in the thresholds and gain of the visceral afferent pathways are present in patients with FDBs. This has been referred to as visceral hyperalgesia (Mayer et al., 1994).

[0028] It has been proposed that FDBs are a result of increased excitability of spinal neurones. According to their model, many inputs can result in transient, short term, or life long sensitization of afferent pathways involved in visceral reflexes and sensations from the gut. The increased sensory input to interneurons and / or dorsal horn neurons in the spinal cord will result in secondary hyperalgesia, in which adjacent, undamaged viscera develop sensitivity to normal innocuous stimuli (allodynia), and central hyperexcitability as a consequence of changes in the circuitry of the dorsal horn. This central sensitization may subsequently extend to supraspinal centers also.

[0029] Altered spinal processing of visceral sensory information can explain altered sensory thresholds and altered referral patterns, the perception of visceral sensations without stimulation of visceral mechanoreceptors (sensation of incomplete evacuation), and the symptomatic involvement of multiple sites in the GI tract, including extra intestinal sites. Increased excitability of dorsal horn neurones, resulting in the recruitment of previously sub-

threshold inputs, may explain cutaneous allodynia in some patients with IBS, burning sensations referred to different parts of the body, cold hypersensitivity and pain referral to upper and lower extremities.

[0030] A number of compounds have been shown to modulate visceral sensitivity in IBS patients. These include octreotide ( $\text{sst}_2$ ; Novartis), the 5-HT<sub>3</sub> antagonists odansetron (Glaxo) and granisetron (SKB) and the peripheral kappa opioid agonist, fedotozine (Jouveinal SA). The 5-HT<sub>3</sub> antagonist alosteron (Glaxo), currently in development for IBS, is active in modifying the perception of colonic distension and gut compliance in IBS patients. New drugs in development for the treatment of IBS that are targeted at pain control as well as dysmotility include 5-HT<sub>3</sub> and 5-HT<sub>4</sub> receptor antagonists. 5-HT<sub>3</sub> receptors are located throughout the central and peripheral nervous system – their role in modulating the activity of visceral afferent and enteric neurones has led to the proposal that 5-HT acts as a sensitizing agent via these receptors on visceral afferent neurones. 5-HT<sub>3</sub> receptor antagonists have been widely reported to attenuate blood pressure responses to intestinal distension. 5-HT<sub>3</sub> antagonists in development for IBS include Alosteron (phase III), which is reported to reduce abdominal pain, slow colonic transit and increase colon compliance in IBS patients. Other compounds with positive effects include the antiemetic Ramosteron (Yamanouchi), Cilansteron (Solvay) and YM-114 (Yamanouchi). An animal model for dysmotility of the GI tract has been described by Maric et al. (1989).

[0031] The conotoxin peptides described herein are sufficiently small to be chemically synthesized. General chemical syntheses for preparing the foregoing conotoxin peptides are described hereinafter. Various ones of the conotoxin peptides can also be obtained by isolation and purification from specific *Conus* species using the technique described in U.S. Patent Nos. 4,447,356 (Olivera et al., 1984); 5,514,774; 5,719,264; and 5,591,821, as well as in PCT published application WO 98/03189, the disclosures of which are incorporated herein by reference.

[0032] Although the conotoxin peptides of the present invention can be obtained by purification from cone snails, because the amounts of conotoxin peptides obtainable from individual snails are very small, the desired substantially pure conotoxin peptides are best practically obtained in commercially valuable amounts by chemical synthesis using solid-phase strategy. For example, the yield from a single cone snail may be about 10 micrograms or less of conotoxin peptides peptide. By "substantially pure" is meant that the peptide is present in the substantial absence of other biological molecules of the same type; it is preferably present in an

amount of at least about 85% purity and preferably at least about 95% purity. Chemical synthesis of biologically active conotoxin peptides depends of course upon correct determination of the amino acid sequence.

[0033] The conotoxin peptides can also be produced by recombinant DNA techniques well known in the art. Such techniques are described by Sambrook et al. (1989). A gene of interest (i.e., a gene that encodes a suitable conotoxin peptides) can be inserted into a cloning site of a suitable expression vector by using standard techniques. These techniques are well known to those skilled in the art. The expression vector containing the gene of interest may then be used to transfect the desired cell line. Standard transfection techniques such as calcium phosphate co-precipitation, DEAE-dextran transfection or electroporation may be utilized. A wide variety of host/expression vector combinations may be used to express a gene encoding a conotoxin peptide of interest. Such combinations are well known to a skilled artisan. The peptides produced in this manner are isolated, reduced if necessary, and oxidized to form the correct disulfide bonds.

[0034] One method of forming disulfide bonds in the conotoxin peptides of the present invention is the air oxidation of the linear peptides for prolonged periods under cold room temperatures or at room temperature. This procedure results in the creation of a substantial amount of the bioactive, disulfide-linked peptides. The oxidized peptides are fractionated using reverse-phase high performance liquid chromatography (HPLC) or the like, to separate peptides having different linked configurations. Thereafter, either by comparing these fractions with the elution of the native material or by using a simple assay, the particular fraction having the correct linkage for maximum biological potency is easily determined. However, because of the dilution resulting from the presence of other fractions of less biopotency, a somewhat higher dosage may be required.

[0035] The peptides are synthesized by a suitable method, such as by exclusively solid-phase techniques, by partial solid-phase techniques, by fragment condensation or by classical solution couplings.

[0036] In conventional solution phase peptide synthesis, the peptide chain can be prepared by a series of coupling reactions in which constituent amino acids are added to the growing peptide chain in the desired sequence. Use of various coupling reagents, e.g., dicyclohexylcarbodiimide or diisopropylcarbonyldimidazole, various active esters, e.g., esters of N-hydroxyphthalimide or N-hydroxy-succinimide, and the various cleavage reagents, to carry

out reaction in solution, with subsequent isolation and purification of intermediates, is well known classical peptide methodology. Classical solution synthesis is described in detail in the treatise, "Methoden der Organischen Chemie (Houben-Weyl): Synthese von Peptiden," (1974). Techniques of exclusively solid-phase synthesis are set forth in the textbook, "Solid-Phase Peptide Synthesis," (Stewart and Young, 1969), and are exemplified by the disclosure of U.S. Patent 4,105,603 (Vale et al., 1978). The fragment condensation method of synthesis is exemplified in U.S. Patent 3,972,859 (1976). Other available syntheses are exemplified by U.S. Patents No. 3,842,067 (1974) and 3,862,925 (1975). The synthesis of peptides containing  $\gamma$ -carboxyglutamic acid residues is exemplified by Rivier et al. (1987), Nishiuchi et al. (1993) and Zhou et al. (1996).

[0037] Common to such chemical syntheses is the protection of the labile side chain groups of the various amino acid moieties with suitable protecting groups which will prevent a chemical reaction from occurring at that site until the group is ultimately removed. Usually also common is the protection of an  $\alpha$ -amino group on an amino acid or a fragment while that entity reacts at the carboxyl group, followed by the selective removal of the  $\alpha$ -amino protecting group to allow subsequent reaction to take place at that location. Accordingly, it is common that, as a step in such a synthesis, an intermediate compound is produced which includes each of the amino acid residues located in its desired sequence in the peptide chain with appropriate side-chain protecting groups linked to various ones of the residues having labile side chains.

[0038] As far as the selection of a side chain amino protecting group is concerned, generally one is chosen which is not removed during deprotection of the  $\alpha$ -amino groups during the synthesis. However, for some amino acids, e.g., His, protection is not generally necessary. In selecting a particular side chain protecting group to be used in the synthesis of the peptides, the following general rules are followed: (a) the protecting group preferably retains its protecting properties and is not split off under coupling conditions, (b) the protecting group should be stable under the reaction conditions selected for removing the  $\alpha$ -amino protecting group at each step of the synthesis, and (c) the side chain protecting group must be removable, upon the completion of the synthesis containing the desired amino acid sequence, under reaction conditions that will not undesirably alter the peptide chain.

[0039] It should be possible to prepare many, or even all, of these peptides using recombinant DNA technology. However, when peptides are not so prepared, they are preferably prepared using the Merrifield solid-phase synthesis, although other equivalent chemical

syntheses known in the art can also be used as previously mentioned. Solid-phase synthesis is commenced from the C-terminus of the peptide by coupling a protected  $\alpha$ -amino acid to a suitable resin. Such a starting material can be prepared by attaching an  $\alpha$ -amino-protected amino acid by an ester linkage to a chloromethylated resin or a hydroxymethyl resin, or by an amide bond to a benzhydrylamine (BHA) resin or paramethylbenzhydrylamine (MBHA) resin. Preparation of the hydroxymethyl resin is described by Bodansky et al. (1966). Chloromethylated resins are commercially available from Bio Rad Laboratories (Richmond, CA) and from Lab. Systems, Inc. The preparation of such a resin is described by Stewart and Young (1969). BHA and MBHA resin supports are commercially available, and are generally used when the desired polypeptide being synthesized has an unsubstituted amide at the C-terminus. Thus, solid resin supports may be any of those known in the art, such as one having the formulae  $-O-CH_2$ -resin support,  $-NH$  BHA resin support, or  $-NH$ -MBHA resin support. When the unsubstituted amide is desired, use of a BHA or MBHA resin is preferred, because cleavage directly gives the amide. In case the N-methyl amide is desired, it can be generated from an N-methyl BHA resin. Should other substituted amides be desired, the teaching of U.S. Patent No. 4,569,967 (Kornreich et al., 1986) can be used, or should still other groups than the free acid be desired at the C-terminus, it may be preferable to synthesize the peptide using classical methods as set forth in the Houben-Weyl text (1974).

[0040] The C-terminal amino acid, protected by Boc or Fmoc and by a side-chain protecting group, if appropriate, can be first coupled to a chloromethylated resin according to the procedure set forth in K. Horiki et al. (1978), using KF in DMF at about 60°C for 24 hours with stirring, when a peptide having free acid at the C-terminus is to be synthesized. Following the coupling of the BOC-protected amino acid to the resin support, the  $\alpha$ -amino protecting group is removed, as by using trifluoroacetic acid (TFA) in methylene chloride or TFA alone. The deprotection is carried out at a temperature between about 0°C and room temperature. Other standard cleaving reagents, such as HCl in dioxane, and conditions for removal of specific  $\alpha$ -amino protecting groups may be used as described in Schroder & Lubke (1965).

[0041] After removal of the  $\alpha$ -amino-protecting group, the remaining  $\alpha$ -amino- and side chain-protected amino acids are coupled step-wise in the desired order to obtain the intermediate compound defined hereinbefore, or as an alternative to adding each amino acid separately in the synthesis, some of them may be coupled to one another prior to addition to the solid phase reactor. Selection of an appropriate coupling reagent is within the skill of the art. Particularly

suitable as a coupling reagent is N,N'-dicyclohexylcarbodiimide (DCC, DIC, HBTU, HATU, TBTU in the presence of HoBt or HoAt).

[0042] The activating reagents used in the solid phase synthesis of the peptides are well known in the peptide art. Examples of suitable activating reagents are carbodiimides, such as N,N'-diisopropylcarbodiimide and N-ethyl-N'-(3-dimethylaminopropyl)carbodiimide. Other activating reagents and their use in peptide coupling are described by Schroder & Lubke (1965) and Kapoor (1970).

[0043] Each protected amino acid or amino acid sequence is introduced into the solid-phase reactor in about a twofold or more excess, and the coupling may be carried out in a medium of dimethylformamide (DMF):CH<sub>2</sub>Cl<sub>2</sub> (1:1) or in DMF or CH<sub>2</sub>Cl<sub>2</sub> alone. In cases where intermediate coupling occurs, the coupling procedure is repeated before removal of the  $\alpha$ -amino protecting group prior to the coupling of the next amino acid. The success of the coupling reaction at each stage of the synthesis, if performed manually, is preferably monitored by the ninhydrin reaction, as described by Kaiser et al. (1970). Coupling reactions can be performed automatically, as on a Beckman 990 automatic synthesizer, using a program such as that reported in Rivier et al. (1978).

[0044] After the desired amino acid sequence has been completed, the intermediate peptide can be removed from the resin support by treatment with a reagent, such as liquid hydrogen fluoride or TFA (if using Fmoc chemistry), which not only cleaves the peptide from the resin but also cleaves all remaining side chain protecting groups and also the  $\alpha$ -amino protecting group at the N-terminus if it was not previously removed to obtain the peptide in the form of the free acid. If Met is present in the sequence, the Boc protecting group is preferably first removed using trifluoroacetic acid (TFA)/ethanedithiol prior to cleaving the peptide from the resin with HF to eliminate potential S-alkylation. When using hydrogen fluoride or TFA for cleaving, one or more scavengers such as anisole, cresol, dimethyl sulfide and methylethyl sulfide are included in the reaction vessel.

[0045] Cyclization of the linear peptide is preferably affected, as opposed to cyclizing the peptide while a part of the peptide-resin, to create bonds between Cys residues. To effect such a disulfide cyclizing linkage, fully protected peptide can be cleaved from a hydroxymethylated resin or a chloromethylated resin support by ammonolysis, as is well known in the art, to yield the fully protected amide intermediate, which is thereafter suitably cyclized and deprotected. Alternatively, deprotection, as well as cleavage of the peptide from the above

resins or a benzhydrylamine (BHA) resin or a methylbenzhydrylamine (MBHA), can take place at 0°C with hydrofluoric acid (HF) or TFA, followed by oxidation as described above.

[0046] The peptides are also synthesized using an automatic synthesizer. Amino acids are sequentially coupled to an MBHA Rink resin (typically 100 mg of resin) beginning at the C-terminus using an Advanced Chemtech 357 Automatic Peptide Synthesizer. Couplings are carried out using 1,3-diisopropylcarbodiimide in N-methylpyrrolidinone (NMP) or by 2-(1H-benzotriazole-1-yl)-1,1,3,3-tetramethyluronium hexafluorophosphate (HBTU) and diethylisopropylethylamine (DIEA). The Fmoc protecting group is removed by treatment with a 20% solution of piperidine in dimethylformamide(DMF). Resins are subsequently washed with DMF (twice), followed by methanol and NMP.

[0047] Muteins, analogs or active fragments, of the foregoing conotoxin peptides are also contemplated here. See, e.g., Hammerland et al. (1992). Derivative muteins, analogs or active fragments of the conotoxin peptides may be synthesized according to known techniques, including conservative amino acid substitutions, such as outlined in U.S. Patent Nos. 5,545,723 (see particularly col. 2, line 50--col. 3, line 8); 5,534,615 (see particularly col. 19, line 45--col. 22, line 33); and 5,364,769 (see particularly col. 4, line 55--col. 7, line 26), each herein incorporated by reference.

[0048] Pharmaceutical compositions containing a compound of the present invention as the active ingredient can be prepared according to conventional pharmaceutical compounding techniques. See, for example, *Remington's Pharmaceutical Sciences*, 18th Ed. (1990, Mack Publishing Co., Easton, PA). Typically, an antagonistic amount of active ingredient will be admixed with a pharmaceutically acceptable carrier. The carrier may take a wide variety of forms depending on the form of preparation desired for administration, e.g., intravenous, oral, parenteral or intrathecally. For examples of delivery methods see U.S. Patent No. 5,844,077, incorporated herein by reference.

[0049] "Pharmaceutical composition" means physically discrete coherent portions suitable for medical administration. "Pharmaceutical composition in dosage unit form" means physically discrete coherent units suitable for medical administration, each containing a daily dose or a multiple (up to four times) or a sub-multiple (down to a fortieth) of a daily dose of the active compound in association with a carrier and/or enclosed within an envelope. Whether the composition contains a daily dose, or for example, a half, a third or a quarter of a daily dose, will

depend on whether the pharmaceutical composition is to be administered once or, for example, twice, three times or four times a day, respectively.

[0050] The term "salt", as used herein, denotes acidic and/or basic salts, formed with inorganic or organic acids and/or bases, preferably basic salts. While pharmaceutically acceptable salts are preferred, particularly when employing the compounds of the invention as medicaments, other salts find utility, for example, in processing these compounds, or where non-medicament-type uses are contemplated. Salts of these compounds may be prepared by art-recognized techniques.

[0051] Examples of such pharmaceutically acceptable salts include, but are not limited to, inorganic and organic addition salts, such as hydrochloride, sulphates, nitrates or phosphates and acetates, trifluoroacetates, propionates, succinates, benzoates, citrates, tartrates, fumarates, maleates, methane-sulfonates, isothionates, theophylline acetates, salicylates, respectively, or the like. Lower alkyl quaternary ammonium salts and the like are suitable, as well.

[0052] As used herein, the term "pharmaceutically acceptable" carrier means a non-toxic, inert solid, semi-solid liquid filler, diluent, encapsulating material, formulation auxiliary of any type, or simply a sterile aqueous medium, such as saline. Some examples of the materials that can serve as pharmaceutically acceptable carriers are sugars, such as lactose, glucose and sucrose, starches such as corn starch and potato starch, cellulose and its derivatives such as sodium carboxymethyl cellulose, ethyl cellulose and cellulose acetate; powdered tragacanth; malt, gelatin, talc; excipients such as cocoa butter and suppository waxes; oils such as peanut oil, cottonseed oil, safflower oil, sesame oil, olive oil, corn oil and soybean oil; glycols, such as propylene glycol, polyols such as glycerin, sorbitol, mannitol and polyethylene glycol; esters such as ethyl oleate and ethyl laurate, agar; buffering agents such as magnesium hydroxide and aluminum hydroxide; alginic acid; pyrogen-free water; isotonic saline, Ringer's solution; ethyl alcohol and phosphate buffer solutions, as well as other non-toxic compatible substances used in pharmaceutical formulations.

[0053] Wetting agents, emulsifiers and lubricants such as sodium lauryl sulfate and magnesium stearate, as well as coloring agents, releasing agents, coating agents, sweetening, flavoring and perfuming agents, preservatives and antioxidants can also be present in the composition, according to the judgment of the formulator. Examples of pharmaceutically acceptable antioxidants include, but are not limited to, water soluble antioxidants such as ascorbic acid, cysteine hydrochloride, sodium bisulfite, sodium metabisulfite, sodium sulfite,

and the like; oil soluble antioxidants, such as ascorbyl palmitate, butylated hydroxyanisole (BHA), butylated hydroxytoluene (BHT), lecithin, propyl gallate, alpha-tocopherol and the like; and the metal chelating agents such as citric acid, ethylenediamine tetraacetic acid (EDTA), sorbitol, tartaric acid, phosphoric acid and the like.

5 [0054] For oral administration, the compounds can be formulated into solid or liquid preparations such as capsules, pills, tablets, lozenges, melts, powders, suspensions or emulsions.

In preparing the compositions in oral dosage form, any of the usual pharmaceutical media may be employed, such as, for example, water, glycols, oils, alcohols, flavoring agents, preservatives, coloring agents, suspending agents, and the like in the case of oral liquid preparations (such as, for example, suspensions, elixirs and solutions); or carriers such as starches, sugars, diluents, granulating agents, lubricants, binders, disintegrating agents and the like in the case of oral solid preparations (such as, for example, powders, capsules and tablets). Because of their ease in administration, tablets and capsules represent the most advantageous oral dosage unit form, in which case solid pharmaceutical carriers are obviously employed. If desired, tablets may be sugar-coated or enteric-coated by standard techniques. The active agent can be encapsulated to make it stable to passage through the gastrointestinal tract while at the same time allowing for passage across the blood brain barrier. See for example, WO 96/11698.

[0055] For parenteral administration, the compound may be dissolved in a pharmaceutical carrier and administered as either a solution or a suspension. Illustrative of suitable carriers are water, saline, dextrose solutions, fructose solutions, ethanol, or oils of animal, vegetative or synthetic origin. The carrier may also contain other ingredients, for example, preservatives, suspending agents, solubilizing agents, buffers and the like. When the compounds are being administered intrathecally, they may also be dissolved in cerebrospinal fluid.

20 [0056] A variety of administration routes are available. The particular mode selected will depend of course, upon the particular drug selected, the severity of the disease state being treated and the dosage required for therapeutic efficacy. The methods of this invention, generally speaking, may be practiced using any mode of administration that is medically acceptable, meaning any mode that produces effective levels of the active compounds without causing clinically unacceptable adverse effects. Such modes of administration include oral, rectal, sublingual, topical, nasal, transdermal or parenteral routes. The term "parenteral" includes subcutaneous, intravenous, epidural, irrigation, intramuscular, release pumps, or infusion.

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[0057] For example, administration of the active agent according to this invention may be achieved using any suitable delivery means, including:

(a) pump (see, e.g., Luer & Hatton (1993), Zimm et al. (1984) and Ettinger et al. (1978));

(b), microencapsulation (see, e.g., U.S. Patent Nos. 4,352,883; 4,353,888; and 5,084,350);

(c) continuous release polymer implants (see, e.g., U.S. Patent No. 4,883,666);

(d) macroencapsulation (see, e.g., U.S. Patent Nos. 5,284,761, 5,158,881, 4,976,859 and 4,968,733 and published PCT patent applications WO92/19195, WO 95/05452);

(e) naked or unencapsulated cell grafts to the CNS (see, e.g., U.S. Patent Nos. 5,082,670 and 5,618,531);

(f) injection, either subcutaneously, intravenously, intra-arterially, intramuscularly, or to other suitable site; or

(g) oral administration, in capsule, liquid, tablet, pill, or prolonged release formulation.

[0058] In one embodiment of this invention, an active agent is delivered directly into the CNS, preferably to the brain ventricles, brain parenchyma, the intrathecal space or other suitable CNS location, most preferably intrathecally.

[0059] Alternatively, targeting therapies may be used to deliver the active agent more specifically to certain types of cell, by the use of targeting systems such as antibodies or cell specific ligands. Targeting may be desirable for a variety of reasons, e.g. if the agent is unacceptably toxic, or if it would otherwise require too high a dosage, or if it would not otherwise be able to enter the target cells.

[0060] The active agents, which are peptides, can also be administered in a cell based delivery system in which a DNA sequence encoding an active agent is introduced into cells designed for implantation in the body of the patient, especially in the spinal cord region.

Suitable delivery systems are described in U.S. Patent No. 5,550,050 and published PCT Application Nos. WO 92/19195, WO 94/25503, WO 95/01203, WO 95/05452, WO 96/02286, WO 96/02646, WO 96/40871, WO 96/40959 and WO 97/12635. Suitable DNA sequences can be prepared synthetically for each active agent on the basis of the developed sequences and the known genetic code.

[0061] Exemplary methods for administering such muscle relaxant compounds (e.g., so as to achieve sterile or aseptic conditions) will be apparent to the skilled artisan. Certain methods suitable for administering compounds useful according to the present invention are set

forth in Goodman and Gilman's *The Pharmacological Basis of Therapeutics*, 7th Ed. (1985). The administration to the patient can be intermittent; or at a gradual, continuous, constant or controlled rate. Administration can be to a warm-blooded animal (e.g. a mammal, such as a mouse, rat, cat, rabbit, dog, pig, cow or monkey); but advantageously is administered to a human being. Administration occurs after general anesthesia is administered. The frequency of administration normally is determined by an anesthesiologist, and typically varies from patient to patient.

[0062] The active agent is preferably administered in an therapeutically effective amount. By a "therapeutically effective amount" or simply "effective amount" of an active compound is meant a sufficient amount of the compound to treat the desired condition at a reasonable benefit/risk ratio applicable to any medical treatment. The actual amount administered, and the rate and time-course of administration, will depend on the nature and severity of the condition being treated. Prescription of treatment, e.g. decisions on dosage, timing, etc., is within the responsibility of general practitioners or specialists, and typically takes account of the disorder to be treated, the condition of the individual patient, the site of delivery, the method of administration and other factors known to practitioners. Examples of techniques and protocols can be found in *Remington's Pharmaceutical Sciences*.

[0063] Dosage may be adjusted appropriately to achieve desired drug levels, locally or systemically. Typically the active agents of the present invention exhibit their effect at a dosage range from about 0.001 mg/kg to about 250 mg/kg, preferably from about 0.01 mg/kg to about 100 mg/kg of the active ingredient, more preferably from about 0.05 mg/kg to about 75 mg/kg. A suitable dose can be administered in multiple sub-doses per day. Typically, a dose or sub-dose may contain from about 0.1 mg to about 500 mg of the active ingredient per unit dosage form. A more preferred dosage will contain from about 0.5 mg to about 100 mg of active ingredient per unit dosage form. Dosages are generally initiated at lower levels and increased until desired effects are achieved. In the event that the response in a subject is insufficient at such doses, even higher doses (or effective higher doses by a different, more localized delivery route) may be employed to the extent that patient tolerance permits. Continuous dosing over, for example 24 hours or multiple doses per day are contemplated to achieve appropriate systemic levels of compounds.

[0064] Advantageously, the compositions are formulated as dosage units, each unit being adapted to supply a fixed dose of active ingredients. Tablets, coated tablets, capsules, ampoules and suppositories are examples of dosage forms according to the invention.

[0065] It is only necessary that the active ingredient constitute an effective amount, i.e., such that a suitable effective dosage will be consistent with the dosage form employed in single or multiple unit doses. The exact individual dosages, as well as daily dosages, are determined according to standard medical principles under the direction of a physician or veterinarian for use humans or animals.

[0066] The pharmaceutical compositions will generally contain from about 0.0001 to 99 wt. %, preferably about 0.001 to 50 wt. %, more preferably about 0.01 to 10 wt.% of the active ingredient by weight of the total composition. In addition to the active agent, the pharmaceutical compositions and medicaments can also contain other pharmaceutically active compounds. Examples of other pharmaceutically active compounds include, but are not limited to, analgesic agents, cytokines and therapeutic agents in all of the major areas of clinical medicine. When used with other pharmaceutically active compounds, the conopeptides of the present invention may be delivered in the form of drug cocktails. A cocktail is a mixture of any one of the compounds useful with this invention with another drug or agent. In this embodiment, a common administration vehicle (e.g., pill, tablet, implant, pump, injectable solution, etc.) would contain both the instant composition in combination supplementary potentiating agent. The individual drugs of the cocktail are each administered in therapeutically effective amounts. A therapeutically effective amount will be determined by the parameters described above; but, in any event, is that amount which establishes a level of the drugs in the area of body where the drugs are required for a period of time which is effective in attaining the desired effects.

[0067] The present invention also relates to rational drug design for the identification of additional drugs which can be used for the purposes described herein. The goal of rational drug design is to produce structural analogs of biologically active polypeptides of interest or of small molecules with which they interact (e.g., agonists, antagonists, inhibitors) in order to fashion drugs which are, for example, more active or stable forms of the polypeptide, or which, e.g., enhance or interfere with the function of a polypeptide *in vivo*. Several approaches for use in rational drug design include analysis of three-dimensional structure, alanine scans, molecular modeling and use of anti-id antibodies. These techniques are well known to those skilled in the art. Such techniques may include providing atomic coordinates defining a three-dimensional

structure of a protein complex formed by said first polypeptide and said second polypeptide, and designing or selecting compounds capable of interfering with the interaction between a first polypeptide and a second polypeptide based on said atomic coordinates.

[0068] Following identification of a substance which modulates or affects polypeptide activity, the substance may be further investigated. Furthermore, it may be manufactured and/or used in preparation, i.e., manufacture or formulation, or a composition such as a medicament, pharmaceutical composition or drug. These may be administered to individuals.

[0069] A substance identified as a modulator of polypeptide function may be peptide or non-peptide in nature. Non-peptide "small molecules" are often preferred for many *in vivo* pharmaceutical uses. Accordingly, a mimetic or mimic of the substance (particularly if a peptide) may be designed for pharmaceutical use.

[0070] The designing of mimetics to a known pharmaceutically active compound is a known approach to the development of pharmaceuticals based on a "lead" compound. This approach might be desirable where the active compound is difficult or expensive to synthesize or where it is unsuitable for a particular method of administration, e.g., pure peptides are unsuitable active agents for oral compositions as they tend to be quickly degraded by proteases in the alimentary canal. Mimetic design, synthesis and testing is generally used to avoid randomly screening large numbers of molecules for a target property.

[0071] Once the pharmacophore has been found, its structure is modeled according to its physical properties, e.g., stereochemistry, bonding, size and/or charge, using data from a range of sources, e.g., spectroscopic techniques, x-ray diffraction data and NMR. Computational analysis, similarity mapping (which models the charge and/or volume of a pharmacophore, rather than the bonding between atoms) and other techniques can be used in this modeling process.

[0072] A template molecule is then selected, onto which chemical groups that mimic the pharmacophore can be grafted. The template molecule and the chemical groups grafted thereon can be conveniently selected so that the mimetic is easy to synthesize, is likely to be pharmacologically acceptable, and does not degrade *in vivo*, while retaining the biological activity of the lead compound. Alternatively, where the mimetic is peptide-based, further stability can be achieved by cyclizing the peptide, increasing its rigidity. The mimetic or mimetics found by this approach can then be screened to see whether they have the target

property, or to what extent it is exhibited. Further optimization or modification can then be carried out to arrive at one or more final mimetics for *in vivo* or clinical testing.

[0073] The present invention further relates to the use of a labeled (e.g., radiolabel, fluorophore, chromophore or the like) of the conotoxins described herein as a molecular tool both *in vitro* and *in vivo*, for discovery of small molecules that exert their action at or partially at the same functional site as the native toxin and capable of elucidation similar functional responses as the native toxin. In one embodiment, the displacement of a labeled conotoxin from its receptor or other complex by a candidate drug agent is used to identify suitable candidate drugs. In a second embodiment, a biological assay on a test compound to determine the therapeutic activity is conducted and compared to the results obtained from the biological assay of a conotoxin. In a third embodiment, the binding affinity of a small molecule to the receptor of a conotoxin is measured and compared to the binding affinity of a conotoxin to its receptor.

[0074] The practice of the present invention employs, unless otherwise indicated, conventional techniques of chemistry, molecular biology, microbiology, recombinant DNA, genetics, immunology, cell biology, cell culture and transgenic biology, which are within the skill of the art. See, e.g., Maniatis *et al.*, 1982; Sambrook *et al.*, 1989; Ausubel *et al.*, 1992; Glover, 1985; Anand, 1992; Guthrie and Fink, 1991; Harlow and Lane, 1988; Jakoby and Pastan, 1979; *Nucleic Acid Hybridization* (B. D. Hames & S. J. Higgins eds. 1984); *Transcription And Translation* (B. D. Hames & S. J. Higgins eds. 1984); *Culture Of Animal Cells* (R. I. Freshney, Alan R. Liss, Inc., 1987); *Immobilized Cells And Enzymes* (IRL Press, 1986); B. Perbal, *A Practical Guide To Molecular Cloning* (1984); the treatise, *Methods In Enzymology* (Academic Press, Inc., N.Y.); *Gene Transfer Vectors For Mammalian Cells* (J. H. Miller and M. P. Calos eds., 1987, Cold Spring Harbor Laboratory); *Methods In Enzymology*, Vols. 154 and 155 (Wu *et al.* eds.), *Immunochemical Methods In Cell And Molecular Biology* (Mayer and Walker, eds., Academic Press, London, 1987); *Handbook Of Experimental Immunology*, Volumes I-IV (D. M. Weir and C. C. Blackwell, eds., 1986); Riott, *Essential Immunology*, 6th Edition, Blackwell Scientific Publications, Oxford, 1988; Hogan *et al.*, *Manipulating the Mouse Embryo*, (Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1986).

### EXAMPLES

[0075] The present invention is described by reference to the following Examples, which are offered by way of illustration and are not intended to limit the invention in any manner. Standard techniques well known in the art or the techniques specifically described below were utilized.

#### EXAMPLE 1

##### Isolation of Conotoxin Peptides

[0076] Crude venom was extracted from venom ducts (Cruz et al., 1976), and the components were purified as previously described (Cartier et al., 1996). The crude extract from venom ducts was purified by reverse phase liquid chromatography (RPLC) using a Vydac C<sub>18</sub> semi-preparative column (10 x 250 mm). Further purification of bioactive peaks was done on a Vydac C<sub>18</sub> analytical column (4.6 x 220 mm). The effluents were monitored at 220 nm. Peaks were collected, and aliquots were assayed for activity. Throughout purification, HPLC fractions were assayed by means of intracerebral ventricular (i.c.v.) injection into mice (Clark et al., 1981).

[0077] The amino acid sequence of the purified peptides were determined by standard methods. The purified peptides were reduced and alkylated prior to sequencing by automated Edman degradation on an Applied Biosystems 477A Protein Sequencer with a 120A Analyzer (DNA/Peptide Facility, University of Utah) (Martinez et al., 1995; Shon et al., 1994).

[0078] In accordance with this method, the conotoxin peptides described as "isolated" in Table 1 were obtained. These conotoxin peptides, as well as the other conotoxin peptides and the conotoxin peptide precursors set forth in Table 1 are synthesized as described in U.S. Patent No. 5,670,622.

#### EXAMPLE 2

##### Isolation of DNA Encoding Conopeptides

[0079] DNA coding for conotoxin peptides was isolated and cloned in accordance with conventional techniques using general procedures well known in the art, such as described in Olivera et al. (1996), including using primers based on the DNA sequence of known conotoxin peptides. For example, primers based on the DNA sequence for the Contulakin-G propeptide were used to identify contulakin homologs. The propeptides of these contulakin homologs are

homologous on the basis of primer amplification, even though the sequence of the mature toxins are not homologous with the Contulakin-G mature toxin. Alternatively, cDNA libraries was prepared from *Conus* venom duct using conventional techniques. DNA from single clones was amplified by conventional techniques using primers which correspond approximately to the M13 universal priming site and the M13 reverse universal priming site. Clones having a size of approximately 300-500 nucleotides were sequenced and screened for similarity in sequence to known conotoxins. The DNA sequences and encoded propeptide sequences are set forth in Table 1. DNA sequences coding for the mature toxin can also be prepared on the basis of the DNA sequences set forth in Table 1. An alignment of the conopeptides of the present invention is set forth in Tables 2-14.

TABLE 1

**Name:** Af6.1  
**Species:** ammiralis  
**Cloned:** Yes

**DNA Sequence:**

ATCATGGAGAACTGATAATTCTGCTTCTTGTTGCTGCTGTA CTGATGTCGACCCAG  
 GCCCTGGTTGAACGTGCTGGAGAAAACCGCTCAAAGGAGAACATCAATTTTATT  
 AAAAAGAAAGAGAGCTGCTGACAGGGGATGTGGGGCGATTGCAAAGATGGGT  
 TAAACGACATGTTTGCGCCCTCAGAGTGTGTTCTGAGGATTGTGAAGGGAGCTGCACG  
 ATGTGGTGATGACCTCTGACCACAAGCCATCTGACATCACCCTCTCTCTTCAGAG  
 GCTTCAAG (SEQ ID NO:1)

**Translation:**

MEKLIILLVAAVL MSTQALVERAGENRSKENINFLKRKRAADRGMWGDKDGLTTC  
 FAPSECCSEDCGSCMTW (SEQ ID NO:2)

**Toxin Sequence:**

Gly-Met-Xaa4-Gly-Asp-Cys-Lys-Asp-Gly-Leu-Thr-Thr-Cys-Phe-Ala-Xaa3-Ser-Xaa1-Cys-Cys-  
 Ser-Xaa1-Asp-Cys-Xaa1-Gly-Ser-Cys-Thr-Met-Xaa4-<sup>^</sup> (SEQ ID NO:3)

**Name:** Af6.2  
**Species:** ammiralis  
**Cloned:** Yes

**DNA Sequence:**

ATCATGGAGAACTGACAATTCTGCTTCTTGTTGCTGCTGTA CTGATGTCGACCCAG  
 GCCCTGCCTCAAGGTGGTGGAGAAAACGCCCAAGGGAGAAATATCAGATTTTATC  
 AAAAAGAAAGACAAATGCTGAGCGTTGGAGGGAGGGCAGTTGCACCTCTTGTTAG

CGACGTGTACGCAAGACCAGCAATGCTGTACTGATGTTTGTTACAAAAGGGACTAC  
TGCGCCTTGTGGGATGACCGCTGACCACAAGCCATCTGACATCACCCTCTCTGT  
CAGAGTCTTCAAG (SEQ ID NO:4)

5 **Translation:**

MEKLTILLLVAAVLMSTQALPQGGGKEKRPRENIRFLSKRKTNAERWREGSCTSWLATC  
TQDQQCCTDVICYKRDYCALWDDR (SEQ ID NO:5)

**Toxin Sequence:**

10 Xaa4-Arg-Xaa1-Gly-Ser-Cys-Thr-Ser-Xaa4-Leu-Ala-Thr-Cys-Thr-Gln-Asp-Gln-Gln-Cys-Cys-  
Thr-Asp-Val-Cys-Xaa5-Lys-Arg-Asp-Xaa5-Cys-Ala-Leu-Xaa4-Asp-Asp-Arg-^ (SEQ ID NO:6)

**Name:** Af6.3  
**Species:** ammimalis  
**Cloned:** Yes

**DNA Sequence:**

ATCATGCAGAACTGATAATTCTGCTTCTTGTTGCTGCTGTGCTGATGTCGACCCAG  
GCCCTGTTTCAAGAAAAACGCACAATGAAGAAGATCGATTTTATCAAAGGGAAA  
GGCAGATGCTGAGAAGCAGAGGAAGCGCAATTGCTCGGATGATTGGCAGTATTGTG  
AAAGTCCCAGTGACTGCTGTAGTTGGGATTGTGATGTGGTCTGCTCGGGATGAACCT  
TGACCACAAGTCATCCGACATCACCCTCTCCTGTTGAGAGGCTTCAAG (SEQ ID  
NO:7)

**Translation:**

MQKLIILLVAAVLMSTQALFQEKRTMKKIDFLSKGKADAQKQRKRNCSDDWQYCESP  
SDCCSWDCDVVCSG (SEQ ID NO:8)

30 **Toxin Sequence:**

Asn-Cys-Ser-Asp-Asp-Xaa4-Gln-Xaa5-Cys-Xaa1-Ser-Xaa3-Ser-Asp-Cys-Cys-Ser-Xaa4-Asp-  
Cys-Asp-Val-Val-Cys-Ser-# (SEQ ID NO:9)

35 **Name:** Af6.4  
**Species:** ammimalis  
**Cloned:** Yes

**DNA Sequence:**

40 ATCATGCAGAACTGATAATCCTGCTTCTTGTTGCTGCTCTACTGTTGTCGATCCAG  
GCGGTAAATCAAGAAAAACCAACGGGCAAAGATCAACTTGCTTTCAAAGAGAA  
AGCCACCTGCTGAGCGTTGGTGGCGGTGGGAGGATGCATGGCTTGGTTTGGGAAA  
TGTTCGAAGGACTCGGAATGTTGTTCTAATAGTTGTGACATAACGCGCTGCGAGTTA  
ATGCGATTCCCACAGACTGGTGACATCGACACTCTCCTGTTGAGAGTCTTCAAG  
45 (SEQ ID NO:10)

**Translation:**

MQKLIIILLVAALLLSIQAVNQEKHQRAKINLLSKRKPPAERWWRWGGCMAWFGKCS  
KDSECCSNSCDITRCELMRFPDPW (SEQ ID NO:11)

#### Toxin Sequence:

- 5 Xaa4-Xaa4-Arg-Xaa4-Gly-Gly-Cys-Met-Ala-Xaa4-Phe-Gly-Lys-Cys-Ser-Lys-Asp-Ser-Xaa1-  
Cys-Cys-Ser-Asn-Ser-Cys-Asp-Ile-Thr-Arg-Cys-Xaa1-Leu-Met-Arg-Phe-Xaa3-Xaa3-Asp-  
Xaa4-^ (SEQ ID NO:12)

- 10 **Name:** Af6.5  
**Species:** ammiralis  
**Cloned:** Yes

#### DNA Sequence:

ATCATGGAGAACTGACAATCCTGCTTCTTGTGCTGCTGTACTGACGTCGACCCAG  
GCCCTGATTCAAGGTGGTGGAGACGAACGCCAAAAGGCAAAGATCAACTTTCTTTC  
AAGGTCGGACCGCGATTGCAGGGGTTACGATGCGCCGTGTAGCTCTGGCGCGCCAT  
GTTGTGATTGGTGGACATGTTTCAGCACGAACCGGGCGCTGTTTTAGGCTGACCACA  
AGCCATCCGACATCACCACCTCCTCTTCAGAGGCTTCAAG (SEQ ID NO:13)

#### Translation:

MEKLTILLLVAAVLSTQALIQQGGDERQKAKINFLSRSDRDCRGYDAPCSSGAPCCDW  
WTCSARTGRCF (SEQ ID NO:14)

#### Toxin Sequence:

Asp-Cys-Arg-Gly-Xaa5-Asp-Ala-Xaa3-Cys-Ser-Ser-Gly-Ala-Xaa3-Cys-Cys-Asp-Xaa4-Xaa4-  
Thr-Cys-Ser-Ala-Arg-Thr-Gly-Arg-Cys-Phe-^ (SEQ ID NO:15)

- 30 **Name:** Af6.6  
**Species:** ammiralis  
**Cloned:** Yes

#### DNA Sequence:

- 35 ATCATGCAGAACTGACAATTCTGCTTCTTGTGCTGCTGTGCTGATGTCGACCCAG  
GCCGTGCTTCAAGAAAAACGCCAAAGGAGAAGATCAAGTTTTATCAAAGAAAAA  
GACAGATGCTGAGAAGCAGCAGAAGCGCCTTTGCCCGGATTACACGGAGCCTTGTT  
CACATGCCCATGAATGCTGTTTCATGGAATTGTCATAATGGGCACTGCACGGGATGA  
ACTCGGACCACAAGCCATCGACATCATCTCTCTGTTTCAGAGTCTTCAAG (SEQ  
40 ID NO:16)

#### Translation:

MQKLTILLLVAAVLMSTQAVLQEKRPKEKIKFLSKKKTD AEKQKRLCPDYTEPCSHA  
HECCSWNCHNGHCTG (SEQ ID NO:17)

#### Toxin Sequence:

Leu-Cys-Xaa3-Asp-Xaa5-Thr-Xaa1-Xaa3-Cys-Ser-His-Ala-His-Xaa1-Cys-Cys-Ser-Xaa4-Asn-Cys-His-Asn-Gly-His-Cys-Thr-# (SEQ ID NO:18)

5 **Name:** Af6.7  
**Species:** ammiralis  
**Cloned:** Yes

**DNA Sequence:**

10 ATCATGCAGAACTGATAATTCTGCTCCTTGTTGCTGCTGACTGATGTCGACCCAG  
 GCCATGTTTCAAGGTGATGGAGAAAAATCCCGGAAAGCGGAGATCAACTTTTCTAA  
 AACAAGAAATTTGGCGAGAAACAGCAGAAACGCTGCAGTAGTTGGGCAAAAGTATT  
 GTGAAGTTGACTCGGAATGCTGTTCCGAACAGTGTGTAAGGTCTTACTGCGCATGT  
 GGTGATGACCTCTGACCACAAGCCATCCGATATCACCCTCTCTCTTCAGAGACTT  
 CAAG (SEQ ID NO:19)

**Translation:**

MQKLIILLVAAVLMSTQAMFQGDGEKSRKAEINFSKTRNLARNKQKRCSSWAKYCEV  
 DSECCSEQCVRSYCAMW (SEQ ID NO:20)

**Toxin Sequence:**

Cys-Ser-Ser-Xaa4-Ala-Lys-Xaa5-Cys-Xaa1-Val-Asp-Ser-Xaa1-Cys-Cys-Ser-Xaa1-Gln-Cys-Val-Arg-Ser-Xaa5-Cys-Ala-Met-Xaa4-^ (SEQ ID NO:21)

**Name:** Af9.1  
**Species:** ammiralis  
**Cloned:** Yes

**DNA Sequence:**

30 GTTAAAAATGCATCTGTCACTGGCACGCTCAGCTGTTTTGATGTTGCTTCTGCTGTTTG  
 CCTTGGGCAACTTTGTGTGGTCCAGTCAGGACAGATAACAAGAGATGTGGACAAT  
 GGACAGCTCACGGACAACCGCCGTAACTGCAATCGAAGTGGAAGCCAGTGAGTCT  
 CTTTCATGTCACGACGGTCTTGTAACAATTCTTGAATGAGCATTCCGATTGCGAATC  
 35 CCATTGTATTGTCACGTTTACGCGATGCAAAATTATTTTGATATAAACGGATTGAGT  
 TTGCTCGTCAACAAGATGTCGCACTACAGCTCCTCTCTACAGTGTGTACATCGACCA  
 AACGACGCATCTTTTATTTCTTTGCTGTTGTATTGTTTTCTGTGTTTCATAACGTAC  
 AGAGCCCTTTAATTACCTTTACTGCTCTTCACTTAACCTGATAACCGGAAGGTCCAG  
 TGCT (SEQ ID NO:22)

**Translation:**

MHLSLARSAYLMLLLFALGNFVVVQSGQITRDVDNGQLTDNRRNLQSKWKPVSLFM  
 SRRSCNNSCNEHSDCESHCICTFSGCKIILI (SEQ ID NO:23)

**Toxin Sequence:**

45 Ser-Cys-Asn-Asn-Ser-Cys-Asn-Xaa1-His-Ser-Asp-Cys-Xaa1-Ser-His-Cys-Ile-Cys-Thr-Phe-Ser-Gly-Cys-Lys-Ile-Ile-Leu-Ile-^ (SEQ ID NO:24)

100-200-300-400-500-600-700-800-900-1000

**Name:** Af9.2  
**Species:** ammiralis  
**Cloned:** Yes

**DNA Sequence:**

GTTAAATGCATCTGTCACTGGCACGCTTAGCTGTTTTGATGTTGCTTCTGCTGTTTG  
 CCTTGGGCAACTTTGTTGTGGTCCAGTCAGGACAGATAACAAGAGATGTGGACAAT  
 GGACAGCTCACGGACAACCGCCGTAACCTGCAATCGAAGTGGAAGCCAGTGAGTCT  
 CTTCATGTACACGACGGTCTTGTAACAATCTTGCAATGAGCATTCCGATTGCGAATC  
 CCATTGTATTTGCACGTTTAGAGGATGCGGAGCTGTTAATGGTTGAGTTTGCTCGTC  
 AACATGATGTGCGACTACACACTACAGCTCCTCTCTACAGTGTGTACATCGACCAAA  
 CGACGCATCTTTATTTCTTTGTCTGTTGTGTTGTTTCCCTGTGTTTCATAACGTACAG  
 AGCCCTTTAATTACTTTTACTGCTCTTCACTTAACCTGATAACCAGAAGGTCCAGTG  
 CT (SEQ ID NO:25)

**Translation:**

MHLSLARLAVLMLLLLFALGNFVVVQSQQITRDVDNQLTDNRRNLQSKWKPVSLFM  
 SRRSCNNSCNEHSDCESHCICTFRGCGAVNG (SEQ ID NO:26)

**Toxin Sequence:**

Ser-Cys-Asn-Asn-Ser-Cys-Asn-Xaa1-His-Ser-Asp-Cys-Xaa1-Ser-His-Cys-Ile-Cys-Thr-Phe-  
 Arg-Gly-Cys-Gly-Ala-Val-Asn-# (SEQ ID NO:27)

**Name:** Ar6.1  
**Species:** arenatus  
**Cloned:** Yes

**DNA Sequence:**

ACCAAAAACCATCATAAAATGAAACTGACGTGCGTGCGTGATCGCTGTGCTGTTCT  
 CTGACGGCCTGTCAACTCACTACAGCTGATGACTCCAGAGGTACGCAGAAGCATGG  
 TGCCTGAGATCGACCACAAACTCTCCATGTTGACTCGGGGCTGCACGCCTCTGG  
 TGAGTGTGTGGTTATCATGGTCACTGCTGCGATTTTGCGATACGTTTCGGCAATTTA  
 TGTGTGAGTGGCTGACCCGGCATCTGACCTTTCCCCCTTCTTTGCTCCACTATCCTTT  
 TTCTGCCTGAGTCCTCCATACCTGAGAGCTGTCATGAACCACTCAACACCTACTCTT  
 CCGGAGGTTTCTGAGGAGCTGCATTGAAATAAAAGCCGATTGC (SEQ ID NO:28)

**Translation:**

MKLTCVVIVAVLFLTACQLTTADDSRGTKQKHGALRSTTKLSMLTRGCTPPGGVCGYHG  
 HCCDFCDITFGNLCVSG (SEQ ID NO:29)

**Toxin Sequence:**

Gly-Cys-Thr-Xaa3-Xaa3-Gly-Gly-Val-Cys-Gly-Xaa5-His-Gly-His-Cys-Cys-Asp-Phe-Cys-Asp-  
 Thr-Phe-Gly-Asn-Leu-Cys-Val-Ser-# (SEQ ID NO:30)

**Name:** Bromosleeper-Ar1  
**Species:** arenatus  
**Cloned:** Yes

**DNA Sequence:**

GACAGGATTGAACAAAATTCAGGATGTCAGGATTGGGAATCATGGTGCTAACCCCTT  
 CTACTTCTTGTGTTCATGGCAACCAGTCATCAGGATGCAGGAGAGAAGAAGGCGAT  
 GCAAAGGGACGCAATCAACGTCAGACGGAGAAGATCACTCACTCGGGGAGTAGTA  
 ACTGAGGCGTGCGAAGAGTCCTGTGAGGAGGAGGAAAAAGCACTGCTGCCACGTAA  
 ATAATGGAGTACCCTCTTGTGCCGTTATATGCTGGGGATAGTTTCTCGCACACTGTC  
 TCATTCAATTATTTATCAGTACAAGTGTAACGAGACATGTCAGAAAGTCGAAGGTT  
 GTGCGTATTGATAAGTATTGTTTACTGGGATGAACGGA (SEQ ID NO:31)

**Translation:**

MSGLGIMVLTLTLLVFMATSHQDAGEKKAMQRDAINVRRRSLTRGVVTEACEESCEE  
 EEKHCHVNNGVPSCAVICWG (SEQ ID NO:32)

**Toxin Sequence:**

Val-Val-Thr-Xaa1-Ala-Cys-Xaa1-Xaa1-Ser-Cys-Xaa1-Xaa1-Xaa1-Lys-His-Cys-Cys-His-  
 Val-Asn-Asn-Gly-Val-Xaa3-Ser-Cys-Ala-Val-Ile-Cys-Xaa4-# (SEQ ID NO:33)

**Name:** Bromosleeper-Ar1A  
**Species:** arenatus  
**Cloned:** Yes

**DNA Sequence:**

GACAGGATTGAACAAAATTCAGGATGTCAGGATTGGGAATCATGGTGCTAACCCCTT  
 CTACTTCTTGTGTTCATGGCAACCAGTCATCAGGATGCAGGAGAGAAGCAGGCGAC  
 GGAAAGGGACGCAATCAACATCAGATGGAGAAGATCACGCACTCGGAGAATAGTA  
 ACTGAGGCGTGCGAAGAGTCCTGTGAGGACGAGGAAAAAGCACTGCTGCCACGTAA  
 ATAATGGAGTACCCTCTTGTGCCGTTATATGCTGGGGATAGTTTCTCGCACACTGTC  
 TCATTCAATTATTTATCAGTACAAGTGTAACGAGACATGTCAGAAAGTCGAAGGTT  
 GTGCGTATTGATAAGTATTGTTTACTGGGATGAACGGA (SEQ ID NO:34)

**Translation:**

MSGLGIMVLTLTLLVFMATSHQDAGEKQATERDAINIRWRRSRTRIVTEACEESCEDE  
 EKHCHVNNGVPSCAVICWG (SEQ ID NO:35)

**Toxin Sequence:**

Ile-Val-Thr-Xaa1-Ala-Cys-Xaa1-Xaa1-Ser-Cys-Xaa1-Asp-Xaa1-Xaa1-Lys-His-Cys-Cys-His-  
 Val-Asn-Asn-Gly-Val-Xaa3-Ser-Cys-Ala-Val-Ile-Cys-Xaa4-# (SEQ ID NO:36)

**Name:** Bromosleeper-Ar2  
**Species:** arenatus  
**Cloned:** Yes

#### DNA Sequence:

GACAGGATTGAACAAAATTCAGGATGTCAGAACTGGGAATCATGGTGCTAACGCTT  
 CTACTTCTTGTTCTCTGGTAACCAAGTCATCAGGATGCAGGAGAGAAGCAGGCGAC  
 GGAAAGGGACGCAATCAACATCAGATGGAGAAGATCACTCACTCGGAGAATAGTA  
 ACTGAGGCGTGCGAAGAGCACTGTGAGGATGAGGAACAGTTCTGCTGCGGCTTAGA  
 GAATGGACAACCCCTTTGTGCCCTGTTTGTCTCGATAGTTTCTGTACACTGTCTCA  
 TTAATTTATTTATCAGTACAAGTGTAACAAAACATGTCAGAAAGTCGAAGGTTGTG  
 CGTATTTGATAAGTATTGTTTGGTGGGACGAACGGA (SEQ ID NO:37)

#### Translation:

MSELGIMVLTLTLLLVFLVTSHQDAGEKQATERDAINIRWRRSLTRRIVTEACEEHCEDEE  
 QFCCGLENGQPFCAVCFG (SEQ ID NO:38)

#### Toxin Sequence:

Ile-Val-Thr-Xaa1-Ala-Cys-Xaa1-Xaa1-His-Cys-Xaa1-Asp-Xaa1-Xaa1-Gln-Phe-Cys-Cys-Gly-  
 Leu-Xaa1-Asn-Gly-Gln-Xaa3-Phe-Cys-Ala-Xaa3-Val-Cys-Phe-# (SEQ ID NO:39)

**Name:** Bromosleeper-Ar3  
**Species:** arenatus  
**Cloned:** Yes

#### DNA Sequence:

GACAGGATTGAACAAAATTCAGGATGTCAGGATTGGGAATCATGGTGCTAACCCCTT  
 CTACTTCTTGTTTCATGGCAACCAGTCATCAGGATGCAGGAGAGAAGAAGGTGAT  
 GCAAAGGGACGCAATCAACGTCAGACGGAAGATCACGCACTCGGAGAGTAGTA  
 ACTGGGGCGTGCGAAGAGCACTGTGAGGACGAGGAAAAGCACTGCTGCGGCTTAG  
 AGAATGGACAAACCCCTTTGTGCCCGTCTATGCTTAGGATAGTTTCTGTACACTGTCT  
 TATTCATTATTTATCAGTACAAGTGAAAACAAAGCATGTCAGAAAGTCGAAGGTTG  
 TCGTATTTGATAAGTATTGTTTACTGGGATGAACGGA (SEQ ID NO:40)

#### Translation:

MSELGIMVLTLTLLLVFMATSHQDAGEKKVMQRDAINVRRRRSRTRRVVTGACEEHCE  
 DEEKHCCGLENGQPFCAVCLG (SEQ ID NO:41)

#### Toxin Sequence:

Val-Val-Thr-Gly-Ala-Cys-Xaa1-Xaa1-His-Cys-Xaa1-Asp-Xaa1-Xaa1-Lys-His-Cys-Cys-Gly-  
 Leu-Xaa1-Asn-Gly-Gln-Xaa3-Phe-Cys-Ala-Arg-Leu-Cys-Leu-# (SEQ ID NO:42)

**Name:** C. arenatus contryphan 1  
**Species:** arenatus  
**Cloned:** Yes

10075602021140

**DNA Sequence:**

ATGGGGAAACTGACAATACTGGTTCTTGTGCTGCTGTACTGTTGTCGACCCAGGTC  
 ATGGTTCAAGGTGACGGAGATCAACCTGCAGCTCGCAATGCAGTGCCAAAAGACGA  
 TAACCCAGATGGAGCGAGTGGAAAGTTCATGAATGTTCTACGTCGGTCTGGATGTC  
 CGTGGCATCCTTGGTGTGGCTGATCGGAATCCACGATTGCAATGACAGCC (SEQ ID  
 NO:43)

**Translation:**

MGKLTILVLVAAVLLSTQVMVQGDGDQPAARNAVPKDDNPDGASGKFMNVLRRSGCP  
 WHPWCG (SEQ ID NO:44)

**Toxin Sequence:**

Ser-Gly-Cys-Xaa3-Xaa4-His-Xaa3-Xaa4-Cys-# (SEQ ID NO:45)

**Name:** C. arenatus contryphan 1A  
**Species:** arenatus  
**Cloned:** Yes

**DNA Sequence:**

ATGGGGAAACTGACAATACTGGTTCTTGTGCTGCTGTACTGTTGTCGACCCAGGTC  
 ATGGTTCAAGGTGACGGAGATCAACCTGCAGCTCGCAATGCAGTGCCAAAAGACGA  
 TAACCCAGATGGAGCGAGTGGAAAGTTCATGAATGTTCTACGTCGGTCTGGATGTC  
 CGTGGCGCCCTTGGTGTGGCTGATCGGAATCCACGATTGCAATGACAGCC (SEQ ID  
 NO:46)

**Translation:**

MGKLTILVLVAAVLLSTQVMVQGDGDQPAARNAVPKDDNPDGASGKFMNVLRRSGCP  
 WRPWCG (SEQ ID NO:47)

**Toxin Sequence:**

Ala-Ser-Gly-Cys-Xaa3-Xaa4-Arg-Xaa3-Xaa4-Cys-# (SEQ ID NO:48)

**Name:** C. arenatus contryphan 2  
**Species:** arenatus  
**Cloned:** Yes

**DNA Sequence:**

ATGGGGAAACTGACAATACTGGTTCTTGTGCTGCTGTACTGTTGTCGACCCAGGTC  
 ATGGTTCAAGGTGACGGAGATCAACCTGCAGGTGAGATGCAGTTCCAAGAGACGA  
 TAACCCAGGTGGAACGAGTGGAAAGTTCATGAATGCTCTACGTCAATATGGATGTC  
 CGGTGGGTCTTTGGTGTGACTGATCAGAATCCACGATTGCAATGACAGCC (SEQ ID  
 NO:49)

**Translation:**

MGKLTILVLVAAVLLSTQVMVQGDGDQPAGRDAVPRDDNPGGTSGKFMNALRQYGC  
PVGLWCD (SEQ ID NO:50)

**Toxin Sequence:**

5 Xaa2-Xaa5-Gly-Cys-Xaa3-Val-Gly-Leu-Xaa4-Cys-Asp-^ (SEQ ID NO:51)

**Name:** C. arenatus contryphan 4

**Species:** arenatus

**Cloned:** Yes

**DNA Sequence:**

ATGGGGAAACTGACAATACTGGTTCCTGTTGCTGCTGTACTGTTGTGCGACCCAGGTC  
ATGTTTCGAGATCAACCTGCACGTCGTGATGCAGTGCCAAGAGACGATAGCCCAGA  
TGAATGAGTGGAGGGTTCATGAATGTCCACGTCGGTCTGGATGTCCTGGCAAC  
CTTGGTGTGGCTGATCGGAATCCACGATTGCAATGACAGCC (SEQ ID NO:52)

**Translation:**

MGKLTILVLVAAVLLSTQVMFRDQPARRDAVPRDDSPDGMSSGGMNVPRRSGCPWQP  
WCG (SEQ ID NO:53)

**Toxin Sequence:**

Ser-Gly-Cys-Xaa3-Xaa4-Gln-Xaa3-Xaa4-Cys-# (SEQ ID NO:54)

**Name:** Contryphan-Ar-1

**Species:** arenatus

**Cloned:** Yes

**DNA Sequence:**

ATGGGGAAACTGACAATACTGGTTCCTGTTGCTGCTGTACTGTTGTGCGACCCAGGCC  
ATGGTTCAAGATCAACCTGCAGGTCGAGATGCAGITCCAAGAGACGATAACCCAGG  
TGGAACGAGTGGAAAAGTTCGTGAATGCTCAACGTCAATATGGATGTCCGCCGGGTC  
TTTGGTGTCACTGATCAGAATCCACGATTGCAATGACAGCC (SEQ ID NO:55)

**Translation:**

MGKLTILVLVAAVLLSTQAMVQDQPAGRDAVPRDDNPGGTSGKFVNAQRQYGCPPGL  
WCH (SEQ ID NO:56)

**Toxin Sequence:**

Xaa2-Xaa5-Gly-Cys-Xaa3-Xaa3-Gly-Leu-Xaa4-Cys-His-^ (SEQ ID NO:57)

**Name:** A10.1

**Species:** aurisiacus

**Cloned:** Yes

**DNA Sequence:**

ATGTTACCGTGTCTTCTGTTGGTTGTCTTGGCAACCACTGTCGTTTCCATCCCTTCAG  
 ATCGTGTCATCTGATGGCAGGAATGCCGCAGTCAACGAGAGAGCGCCTTGGCTGGTC  
 CCTTCGACAATCACGACTTGCTGTGGATATAATCCGGGGACAATGTGCCCTCCTTGC  
 AGGTGCGATAATACCTGTTAACCAAAAAAAAAAAAAAAAAAAAAA (SEQ ID NO:58)

**Translation:**

MFTVFLLVVLATTVVSIPSDRASDGRNAAVNERAPWLVPSTITTCGGYNPGTMCPPCRC  
 DNTC (SEQ ID NO:59)

**Toxin Sequence:**

Ala-Xaa3-Xaa4-Leu-Val-Xaa3-Ser-Thr-Ile-Thr-Thr-Cys-Cys-Gly-Xaa5-Asn-Xaa3-Gly-Thr-  
 Met-Cys-Xaa3-Xaa3-Cys-Arg-Cys-Asp-Asn-Thr-Cys-^ (SEQ ID NO:60)

**Name:** Bn1.5  
**Species:** bandanus  
**Cloned:** Yes

**DNA Sequence:**

ATGCGCTGTCTCCAGTCTTGATCATTCTTCTGCTGCTGACTGCATCTGCACCTGGCG  
 TTGATGTCTACCGAAGACCGAAGATGATGTGCCCTGTCTGTCTACGATAATA  
 CAAAGAGTATCCTACGAGGACTTCTGGACAAACGTGCTTGTGTGGCTACAAGCTT  
 GCTCACCATGTTAACCAAGCATGAAGGATCC (SEQ ID NO:61)

**Translation:**

MRCLPVLHLLLLTASAPGVDVLPKTEDDVPLSSVYDNTKSILRGLLDKRACCGYKLCSP  
 C (SEQ ID NO:62)

**Toxin Sequence:**

Ala-Cys-Cys-Gly-Xaa5-Lys-Leu-Cys-Ser-Xaa3-Cys-^ (SEQ ID NO:63)

**Name:** Ca6.3  
**Species:** characteristic  
**Cloned:** Yes

**DNA Sequence:**

GGATCCATGAACTGACGTGCGTGGTGATCATCGCCGCGCTGTTCTGACGGCCTGT  
 CAGCTCAATACAGCTGATGACTCCAGAGATAAGCAGGAGTACCGTGCAGTGAGGTT  
 GAGAGACGGAATGCGGAATTTCAAAGGTTCCAAGCGCAACTGCGGGGAACAAGGT  
 GAAGGTTGTGCTACTCGCCCATGCTGCTCTGGTCTGAGTTGCGTTGGCAGCCGTCCA  
 GGAGGCTGTGCCAGTACGGCTAATAGTCTGGCATCTGATATTTCCCTCTGCACTC  
 TACCTTCTTTGGCTGATGCATGTTTACTTGTGTGTTGTCATGAACCACTCAGTAGCT  
 ACACCTCCGAAGGACGTGC (SEQ ID NO:64)

**Translation:**

MKLTCVVIIAALFLTACQLNTADDSRDKQEYRAVRLRDGMRNFKGSKRNCGEQEGEC  
 ATRPCCSGLSCVGSRPGLCQYG (SEQ ID NO:65)

**Toxin Sequence:**

Asn-Cys-Gly-Xaa1-Gln-Gly-Xaa1-Gly-Cys-Ala-Thr-Arg-Xaa3-Cys-Cys-Ser-Gly-Leu-Ser-Cys-  
 Val-Gly-Ser-Arg-Xaa3-Gly-Gly-Leu-Cys-Gln-Xaa5-# (SEQ ID NO:66)

**Name:** Ca8.1  
**Species:** characteristic  
**Cloned:** Yes

**DNA Sequence:**

ATGATGTCGAAAAATGGGAGCTATGTTTGTCTTTTGTCTTCTTTTCATCCTGCCATCCA  
 GCCAGCAGGAAGGAGATGTCCAGGCAAGAAAAACGCACCTGAAGAGAGGCTTCTA  
 CGGTA CTCTGGCAATGTCTACCAGAGGATGCTCTGGCACTTGCCATCGTCGTGAGGA  
 CGGCAAGTGTCTGGGGTACTTGC GACTGCTCCGGATACAGCTATTGTCGCTGCGGTGA  
 CGCTCACCATTTTTACCGAGGATGCACGTGTTCTGTCAAGGTTGATTAATTGACTC  
 TTTAACTCGTTGAACGATTGAAAAAAAATTTTAGAGCAATATGTTTCGAGAAAA  
 ACCGAAGAC (SEQ ID NO:67)

**Translation:**

MMSKMGAMFVLLLLFILPSSQEGDVQARKTHLKRGFYGTLAMSTRGCSGTCHRRRED  
 GKCRGTCDCSGYSYCRCGDAHHFYRGCTCSCQG (SEQ ID NO:68)

**Toxin Sequence:**

Gly-Cys-Ser-Gly-Thr-Cys-His-Arg-Arg-Xaa1-Asp-Gly-Lys-Cys-Arg-Gly-Thr-Cys-Asp-Cys-  
 Ser-Gly-Xaa5-Ser-Xaa5-Cys-Arg-Cys-Gly-Asp-Ala-His-His-Phe-Xaa5-Arg-Gly-Cys-Thr-Cys-  
 Ser-Cys-Gln-# (SEQ ID NO:69)

**Name:** Ca8.2  
**Species:** characteristic  
**Cloned:** Yes

**DNA Sequence:**

ATGATGTCGAAAAATGGGAGCTATGTTTGTCTTTTGTCTTCTTTTCATCCTGCCATCCA  
 GCCAGCAGGAAGGAGATGTCCAGGCAAGAAAAACGCACCGGAAGAGCGGCTTCTA  
 CGGTA CTCTGGCAATGTCTGCCAGAGGATGCTCTGGCACTTGCCATCGTCGTGAGGA  
 CGGCAAGTGTCTGGGGTACTTGC GACTGCTCCGGATACAGCTATTGTCGCTGCGGTGA  
 CGCTCACCATTTTTACCGAGGATGCACGTGTACATGTTAAGGTTGATTAATTGACTC  
 TTTAACTCGTTGAACCGATTAAAAAAAATTTAGACGAATATGTTTCGAGAAAACC  
 GAAGAC (SEQ ID NO:70)

**Translation:**

MMSKMGAMFVLLLLFILPSSQEGDVQARKTHRKSGFYGTLAMARGCSGTCHRRER  
GKCRGTCDCSGYSYRCGDAHHFYRGCTCTC (SEQ ID NO:71)

#### Toxin Sequence:

Gly-Cys-Ser-Gly-Thr-Cys-His-Arg-Arg-Xaa1-Asp-Gly-Lys-Cys-Arg-Gly-Thr-Cys-Asp-Cys-  
Ser-Gly-Xaa5-Ser-Xaa5-Cys-Arg-Cys-Gly-Asp-Ala-His-His-Phe-Xaa5-Arg-Gly-Cys-Thr-Cys-  
Thr-Cys-^ (SEQ ID NO:72)

**Name:** Ca8.3  
**Species:** characteristicus  
**Cloned:** Yes

#### DNA Sequence:

ATGATGTCGAAATGGGAGCTATGTTTGTCTTTTGTCTCTTTTCATCCTGCCATCCA  
GCCAGCAGGAAGGAGATGTCCAGGCAAGAAAAACGCACCGGAAGAGCGGCTTCTA  
CGGTACTCTGGCAATGTCTACCAGAGGATGCTCTGGCACTTGCCGTCGTCATCGGGA  
CGGCAAGTGTCTGGGGTACTTGCAGCTGCTCCGGATACAGCTATTGTCGCTGCGGTGA  
CGCTCACCATTTTTACCGAGGATGCACGTGTACATGTTAAGGTTGATTAATTGATC  
TTTAACTCGTTGAACGATTAATAAAAAAAAAATTTAGACGAATATGTTTCGAGAAAA  
CCGAAGAC (SEQ ID NO:73)

#### Translation:

MMSKMGAMFVLLLLFILPSSQEGDVQARKTHRKSGFYGTLAMSTRGCSGTCRRHRD  
GKCRGTCDCSGYSYRCGDAHHFYRGCTCTC (SEQ ID NO:74)

#### Toxin Sequence:

Gly-Cys-Ser-Gly-Thr-Cys-Arg-Arg-His-Arg-Asp-Gly-Lys-Cys-Arg-Gly-Thr-Cys-Asp-Cys-Ser-  
Gly-Xaa5-Ser-Xaa5-Cys-Arg-Cys-Gly-Asp-Ala-His-His-Phe-Xaa5-Arg-Gly-Cys-Thr-Cys-Thr-  
Cys-^ (SEQ ID NO:75)

**Name:** Ca8.4  
**Species:** characteristicus  
**Cloned:** Yes

#### DNA Sequence:

ATGATGTCGAAATGGGAGCTATGTTTGTCTTTTGTCTCTTTTCATCCTGCCATCCA  
GCCAGCAGGAAGGAGATGTCCAGGCAAGAAAAACGCACCTGAAGAGAGGCTTCTA  
CGGTACTCTGGCAATGTCTACCAGAGGATGCTCTGGCACTTGCCGTCGTCATCGGGA  
CGGCAAGTGTCTGGGGTACTTGCAGCTGCTCCGGATACAGCTATTGTCGCTGCGGTGA  
CGCTCACCATTTTTACCGAGGATGCACGTGTACATGTTAAGGTTGATTAATTGATC  
TTTAACTCGTTGAACGATTAATAAAAAAAAAATTTAGAGCAATATGTTTCGAGAAAA  
ACCGAAGAC (SEQ ID NO:76)

#### Translation:

MMSKMGAMFVLLLLFILPSSQEGDVQARKTHLKRFGYGTLAMSTRGCSGTCRRHRD  
GKCRGTCDCSGYSYRCRGGDAHHFYRGCTCTC (SEQ ID NO:77)

#### Toxin Sequence:

Gly-Cys-Ser-Gly-Thr-Cys-Arg-Arg-His-Arg-Asp-Gly-Lys-Cys-Arg-Gly-Thr-Cys-Asp-Cys-Ser-  
Gly-Xaa5-Ser-Xaa5-Cys-Arg-Cys-Gly-Asp-Ala-His-His-Phe-Xaa5-Arg-Gly-Cys-Thr-Cys-Thr-  
Cys-^ (SEQ ID NO:78)

**Name:** Ca8.5  
**Species:** characteristicus  
**Cloned:** Yes

#### DNA Sequence:

ATGATGTCGAAATGGGAGCTATGTTTGTCTTTTGTCTTTTACCCTGCCATCCA  
GCCAGCAGGAAGGAGATGTCCAGGCAAGAAAAACGCACCTGAAGAGAGGCTTCTA  
CGGTACTCTGGCAATGTCTTCCAGAGGATGCTCTGGCACTTGCCATCGTCGTGAGGA  
CGGCAAGTGTCTGGGGTACTTGCAGCTGCTCCGGATACAGCTATTGTCGTGCGGTGA  
CGCTCACCATTTTTACCGAGGATGTACGTGTACATGTTAAGGTTGATTAATTGACTC  
TTTAACTCGTTGAACGATTAATAAAAAAATTTAGAGCAATATGTTTCGAGAAAACCG  
AAGAC (SEQ ID NO:79)

#### Translation:

MMSKMGAMFVLLFLFTLPSSQEGDVQARKTHLKRFGYGTLAMSSRGCSGTCHRRD  
GKCRGTCDCSGYSYRCRGGDAHHFYRGCTCTC (SEQ ID NO:80)

#### Toxin Sequence:

Gly-Cys-Ser-Gly-Thr-Cys-His-Arg-Arg-Xaa1-Asp-Gly-Lys-Cys-Arg-Gly-Thr-Cys-Asp-Cys-  
Ser-Gly-Xaa5-Ser-Xaa5-Cys-Arg-Cys-Gly-Asp-Ala-His-His-Phe-Xaa5-Arg-Gly-Cys-Thr-Cys-  
Thr-Cys-^ (SEQ ID NO:81)

**Name:** Ca8.6  
**Species:** characteristicus  
**Cloned:** Yes

#### DNA Sequence:

ATGATGTCGAAATGGGAGCTATGTTTGTCTTTTGTCTTTTTCATCTGCCATCCA  
GCCAGCAGGAAGGAGATGTCCAGGCAAGAAAAACGCACCTGAAGAGCGGCTTCTA  
CGGTACTCTGGCAATGTCTGCCAGAGGATGCTCTGGCACTTGCCATCGTCGTCAAAA  
CGGCGAGTGTCTAGGGTACTTGCAGCTGCGACGGACACGACCATTTGTGACTGCGGTG  
ACACTCTCGGTACTTACTCAGGATGCGTGTGTATATGTTAAGGTTGATTAATTGACT  
CTTTAACTCGTTGAACGATTAATAAAAAAATTTAGAGCAATATGTTTCGAGAAAACCG  
AAGAC (SEQ ID NO:82)

#### Translation:

MMSKMGAMFVLLLLFILPSSSQEGDVQARKTHLKSGFYGLAMSARGCSGTCHRRQN  
GECQGTCDGDGHDHDCGDTLGTYSGCVCIC (SEQ ID NO:83)

#### Toxin Sequence:

- 5 Gly-Cys-Ser-Gly-Thr-Cys-His-Arg-Arg-Gln-Asn-Gly-Xaa1-Cys-Gln-Gly-Thr-Cys-Asp-Cys-  
Asp-Gly-His-Asp-His-Cys-Asp-Cys-Gly-Asp-Thr-Leu-Gly-Thr-Xaa5-Ser-Gly-Cys-Val-Cys-Ile-  
Cys-^ (SEQ ID NO:84)

- 10 **Name:** Ca9.1  
**Species:** characteristicus  
**Cloned:** Yes

#### DNA Sequence:

GTTACAATGCATCTGTCACTGGCAGCTCAGCTGTCTTGATGTTGCTTCTGCTGTTTG  
CCTTGGACAACCTTCGTTGGGGTCCAGCCAGGACAGATAACAAGAGATGTGGACAAC  
CGCCGTAACCGGCAATCGCGATGGAAGCCAAGGAGTCTCTTCAAGTCACTTCATAA  
ACGAGCATCGTGTGGAGGGACTTGCACGGAAAGTGCCGATTGCCCTTCCACGTGTA  
GTACTTGCTTACATGCTCAATGCGAGTCAACATGATGTCGCACTACAGCTCTTCTCT  
ACAGTGTGTACATCGACCGTACGACGCATCTTTATTCTTTGGCTGTTTCATTTCGTT  
TTCTTGTTTCATAACATGCGGAGCCCTTCCGTTACCTCTACTGCTCTACACTTAACC  
TGATAACCAGAAAAATCCAGTACT (SEQ ID NO:85)

#### Translation:

MHLSLARS AVLMLLLL FALDNFVGVPQGQITRDVDNRRNRQSRWKPRSLFKSLHKRAS  
CGGTCTESADCPSTCSTCLHAQCEST (SEQ ID NO:86)

#### Toxin Sequence:

- 30 Ala-Ser-Cys-Gly-Gly-Thr-Cys-Thr-Xaa1-Ser-Ala-Asp-Cys-Xaa3-Ser-Thr-Cys-Ser-Thr-Cys-  
Leu-His-Ala-Gln-Cys-Xaa1-Ser-Thr-^ (SEQ ID NO:87)

- 35 **Name:** Ca9.2  
**Species:** characteristicus  
**Cloned:** Yes

#### DNA Sequence:

40 GTTACAATGCATCTGTCACTGGCAGCTCAGCTGTTTTGATGTTGCTTCTGCTGTTTG  
CCTTGGACAACCTTCGTTGGGGTCCAACCAGGACAGATAAACTAGAGATGTGGACAAC  
CGCCGTAACCTGCAATCGCGATGGAAGCCAAGGAGTCTCTTCAAGTCACTTCATAA  
ACGAGCATCGTGTGGAGGGACTTGCACGGAAAGTGCCGATTGCCCTTCCACGTGTA  
GTACTTGCTTACATGCTCAATGCGAGTGAACATGATGTCGCACTACAGCTCTTCTCT  
ACAGTGTGTACATCGACCGACCGTACGACGCATCTTTATTCTTTGCTGTTTCATT  
CGTTTTCTTGAGTTCATAACATGCGGAGCCCTTCCGTTACCTCTACTGCTCTACACTT  
45 AAGCTGATAACCAGAAAAATCCAGTACT (SEQ ID NO:88)

#### Translation:

**Toxin Sequence:**

Name: Cr10.2

**Cloned:** Yes

tggtgtgtgtgggttgggtccagcatttgatggcaggaatgccgcagtgcaacgagagagcgccct  
tggacgctgtcgTTTTGTCCACCACGAATTGCTGCGGTTATAATACGATGGAATTCTGC  
CCTGCTGACATGTGCACTTATTTCTGTCCAAAAAGAAAAACCCAGGAAAGGGCCG  
CAGAAACCACTGATGCTCCGAGACCCTTGCTGAACCACGACGT (SEQ ID NO:91)

FDGRNAAVNERAPWTVVLSTTNCCGYNTMEFCPACMCTYSCPKKKKPGKGRRNN  
(SEQ ID NO:92)

Ala-Xaa3-Xaa4-Thr-Val-Val-Leu-Ser-Thr-Thr-Asn-Cys-Cys-Gly-Xaa5-Asn-Thr-Met-Xaa1-  
Phe-Cys-Xaa3-Ala-Cys-Met-Cys-Thr-Xaa5-Ser-Cys-Xaa3-Lys-Lys-Lys-Lys-Xaa3-Gly-Lys-  
Gly-Arg-Arg-Asn-Asn-^ (SEQ ID NO:93)

**Species:** consors

**Cloned:** Yes

**Translation:**

GIFVGVQPEQITRDVDKGYSTDDGHDLLSLLKQISLRACTGSCNSDSECYNFCDICIGTRC  
EAOK (SEQ ID NO:94)

Ala-Cys-Thr-Gly-Ser-Cys-Asn-Ser-Asp-Ser-Xaa1-Cys-Xaa5-Asn-Phe-Cys-Asp-Cys-Ile-Gly-  
Thr-Arg-Cys-Xaa1-Ala-Gln-Lys-^ (SEQ ID NO:95)

**Species:** delessertii

**Isolated:** Yes

**Toxin Sequence:**

Ala-Cys-Lys-Xaa3-Lys-Asn-Asn-Leu-Cys-Ala-Ile-Thr-Xaa1-Met-Ala-Xaa1-Cys-Cys-Ser-Gly-Phe-Cys-Leu-Ile-Xaa5-Arg-Cys-^ (SEQ ID NO:96)

**Name:** Bromosleeper-Di1  
**Species:** distans  
**Cloned:** Yes

**DNA Sequence:**

GACAGGATTGAACAAAATTCAGGATGTCAGGATTGGGAATCATGGTGCTAACCCCTT  
 CTACTTCTTGTGCCCATGGCAACCAGTCAACAGGATGGAGGAGAGAAGCAGGCGAT  
 GCAAAGGGACGCAATCAACGTCGCACCAGGAACATCAATCACTCGGAGAAATGTA  
 GATCAGGAGTGCATTGACGCCTGTCAGCTGGAGGACAAGAATTGCTGTGGCAGAAC  
 AGATGGAGAACCCAGATGTGCGAAAAATCTGCCTCGGATAAATTTCTGTACGCTGTCTC  
 ATTCAATTATTTTCATCCGTACGAGTGTAAACGAGACCTATTAGAAAGTCGAAGGTTGT  
 CGGTAATTTGATAAGCATTGTTTGCTGGGACGAACGGA (SEQ ID NO:97)

**Translation:**

MSGLGIMVLTLTLLVPMATSQQDGGEKQAMQRDAINVAPGTSITRRNVDQECIDACQL  
 EDKNCCGRDGDGEPKACICLG (SEQ ID NO:98)

**Toxin Sequence:**

Asn-Val-Asp-Gln-Xaa1-Cys-Ile-Asp-Ala-Cys-Gln-Leu-Xaa1-Asp-Lys-Asn-Cys-Cys-Gly-Arg-Thr-Asp-Gly-Xaa1-Xaa3-Arg-Cys-Ala-Lys-Ile-Cys-Leu-# (SEQ ID NO:99)

**Name:** Bromosleeper-Di2  
**Species:** distans  
**Cloned:** Yes

**DNA Sequence:**

GACAGGATTGAACAAAATTCAGGATGTCAGGATTGGGAATCATGGTGCTAACCCCTT  
 CTACTTCTTGTGCCCATGGCAACCAGTCAACAGGATGGAGGAGAGAAGCAGGCGAT  
 GCAAAGGGACGCAATCAACGTCGCACCAGGAACATCAATCACTCGGACAGAAACA  
 GATCAGGAGTGCATTGACATCTGTAAGCAGGAGGACAAGAAATGCTGCGGCAGATC  
 AAATGGAGAACCCACATGTGCGAAAAATCTGCCTCGGATAAATTTCTGTACGCTGTCTC  
 GTTCATTATTTTCGTACGACGAGTTTAAACGAGACCTATTAGAAAGTCGAAGGTTTCG  
 TGCTTAATTTGATAAGCATTGTTTGCTGGGATGAACGGA (SEQ ID NO:100)

**Translation:**

MSGLGIMVLTLTLLVPMATSQQDGGEKQAMQRDAINVAPGTSITRTETDQECIDICKQE  
 DKKCCGRSNGEPTCAKICLG (SEQ ID NO:101)

**Toxin Sequence:**

Xaa1-Thr-Asp-Gln-Xaa1-Cys-Ile-Asp-Ile-Cys-Lys-Gln-Xaa1-Asp-Lys-Lys-Cys-Cys-Gly-Arg-Ser-Asn-Gly-Xaa1-Xaa3-Thr-Cys-Ala-Lys-Ile-Cys-Leu-# (SEQ ID NO:102)

**Name:** Bromosleeper-Di3  
**Species:** distans  
**Cloned:** Yes

**DNA Sequence:**

GACAGGATTGAACAAAATTTCAGGATGTCAGGATTGGAATCATGGTGCTAACCCCTT  
 CTACTTCTTGTGCCCATGGCAACCAGTCAACAGGATGGAGGAGAGAAGCAGGCGAT  
 GCAAAGGGACGCAATCAACGTTCGCACCAGGAACATCAATCACTCGGAGAGAAACA  
 GATCAGGAGTGCATTGACACCTGTGAGCAGGAGGACAAGAAATGCTGCGGCAGAA  
 CAAATGGAGAACCCGTATGTGCGAAAATCTGCTTCGGATAATTTCTGTACGCTGTCT  
 CATTCTAATTTTCATCAGTACGAGTTTAAACGAGACCTATTAGAAAGTCGAAGGTTT  
 GTGCTTAATTTGATAAGCATTGTTTGCTGGGATGAACGGA (SEQ ID NO:103)

**Translation:**

MSLGLIMVLTLTLLVPMATSQDGGGEKQAMQRDAINVAPGTSITRRETDQECIDTCEQE  
 DKKCCGRNTNGEPPVCAKICFG (SEQ ID NO:104)

**Toxin Sequence:**

Xaa1-Thr-Asp-Gln-Xaa1-Cys-Ile-Asp-Thr-Cys-Xaa1-Gln-Xaa1-Asp-Lys-Lys-Cys-Cys-Gly-  
 Arg-Thr-Asn-Gly-Xaa1-Xaa3-Val-Cys-Ala-Lys-Ile-Cys-Phe-# (SEQ ID NO:105)

**Name:**  $\alpha$ A-EIVB  
**Species:** ermineus  
**Isolated:** Yes  
**Cloned:** Yes

**DNA Sequence:**

ATGTTTACCCGTGTTTCTGTTGGTTGTCTTGGCAACCACTGTCGTTTCCCTTCAC TTCAG  
 ATCGTGCATCGGATGACAGGAATACCAACGACAAAGCATCTCGCCTGCTCTCTCAC  
 GTTGTCAGGGGATGCTGTGGTAAGTATCCCAATGCTGCCTGTCATCCTTGCGGTTGT  
 ACAGTGGGTAGGCCACCGTATTGTGACAGACCCAGTGTTGGAGGACGCTGATGCTC  
 CAGGACCCTCTGAACCACGACGT (SEQ ID NO:106)

**Translation:**

MFTVFLVLVLTATTVVSFTSDRASDDRNNDKASRLLSHVVRGCCGKYPNAACHPCGCT  
 VGRPPYCDRPSGGGR (SEQ ID NO:107)

**Toxin Sequence:**

Gly-Cys-Cys-Gly-Lys-Xaa5-Xaa3-Asn-Ala-Ala-Cys-His-Xaa3-Cys-Gly-Cys-Thr-Val-Gly-Arg-  
 Xaa3-Xaa3-Xaa5-Cys-Asp-Arg-Xaa3-Ser-Gly-Gly-# (SEQ ID NO:108)

**Name:** Ge3.1  
**Species:** generalis  
**Cloned:** Yes

**DNA Sequence:**

GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTCTGTTCTGTTTCCCC  
 TTAGTCTCTTCCACTGGATGGAGAACCACTGTAGACCGACATGCCGAGCATATGC  
 AGGATGACAATTACAGTGCACAGAACCCTGGGTTATTGCCATCAGACAGTGTTC  
 ACGTCTTGCACACTTGGATGCCAGCCTTGTTGCGTCCCCTGATAACGTGTTGATGAC  
 CAACTTTCTCGAG (SEQ ID NO:109)

**Translation:**

GSMSKLGVLITICLVLFPLTALPLDGEQPVDRHAEHMQDDNSAAQNPVVIARQCCT  
 FCNFGCQPCCV (SEQ ID NO:110)

**Toxin Sequence:**

Xaa2-Cys-Cys-Thr-Phe-Cys-Asn-Phe-Gly-Cys-Gln-Xaa3-Cys-Cys-Val-Xaa3-<sup>^</sup> (SEQ ID NO:111)

**Name:** C. geographus GS-A  
**Species:** geographus  
**Cloned:** Yes

**DNA Sequence:**

GCAAGATCATCAGCAGAATGAACCTGACGTGCGTGTGATCATCGCCGTGCTGTTTC  
 TGACGGCCTGCCAGCTCATTGCAGCTGATGACTCCAGAGATAACCAGAAAGCACCGT  
 GCAGTGAGGATGAGAGACGCATTGAAGAATTTCAAAGATTCAGGGCGTGTCTCCGG  
 TAGAGGTTCTAGATGTCCTCCCAATGCTGCATGGGTTTGACGTGCGGTGCTGAGTA  
 TCCACCCAGATGCGGTTGATATACGGTGAACAACCTGATATTTCCCTCTGTGCTCTA  
 CCCTCTTTTGCCTGATTACCCACACCTATGTGTGGTCATGAACCACTCAGTACCTA  
 CACCTCTGGTGGCTTCAGAGGACGTATATTAATAAATAAACACATTGCAATGAAAA  
 AAAAAAA (SEQ ID NO:112)

**Translation:**

MNLTCLVLIIVLFTACQLIAADDSRDNQKHRAVRMRDALKNFKDSRACSGRGRCP  
 QCCMGLTCGREYPPRCG (SEQ ID NO:113)

**Toxin Sequence:**

Ala-Cys-Ser-Gly-Arg-Gly-Ser-Arg-Cys-Xaa3-Xaa3-Gln-Cys-Cys-Met-Gly-Leu-Thr-Cys-Gly-  
 Arg-Xaa1-Xaa5-Xaa3-Xaa3-Arg-Cys-# (SEQ ID NO:114)

**Name:** Conopressin-G  
**Species:** geographus  
**Isolated:** Yes

**Toxin Sequence:**

Cys-Phe-Ile-Arg-Asn-Cys-Xaa3-Lys-Gly-# (SEQ ID NO:115)

**Name:** EST66  
**Species:** geographus  
**Cloned:** Yes

**DNA Sequence:**

TGCTGCCCGAGTAGCAAAGAGGATTCCCTGAACTGCATTGAGACCATGGCGACCAC  
 GGCCACGTGCATGAAGTCCAACAAGGGGGAGATCTACTCCTATGCGTGCGGCTACT  
 GCGGCAAGAAGAAGGAGAGCTGTTTCGGCGACAAAAAGCCAGTGACTGACTACCA  
 GTGCCAGACGCGGAACATTCCCAACCCCTGCGGCGGCGTGCTCTCTGAAGGCACC  
 AACAGCACCAACAGCACGATCTCCTGTGTTTCGTCACTGCATTATGACGTCAAAAC  
 CACGTCAATGCATGATGACGACGATCTCGGCTATGGCATGTATTGAAGAATGGAAAT  
 AAACCTAGTTTTCAGCTGAAAAAA (SEQ ID NO:116)

**Translation:**

CCPSSKEDSLNCIETMATTATCMKSNKGEIYSYACGYCGKKKESCFGDKKPVTDYQCQ  
 TRNIPNPCGGAAL (SEQ ID NO:117)

**Toxin Sequence:**

Cys-Cys-Xaa3-Ser-Ser-Lys-Xaa1-Asp-Ser-Leu-Asn-Cys-Ile-Xaa1-Thr-Met-Ala-Thr-Thr-Ala-  
 Thr-Cys-Met-Lys-Ser-Asn-Lys-Gly-Xaa1-Ile-Xaa5-Ser-Xaa5-Ala-Cys-Gly-Xaa5-Cys-Gly-Lys-  
 Lys-Lys-Xaa1-Ser-Cys-Phe-Gly-Asp-Lys-Lys-Xaa3-Val-Thr-Asp-Xaa5-Gln-Cys-Gln-Thr-Arg-  
 Asn-Ile-Xaa3-Asn-Xaa3-Cys-Gly-Gly-Ala-Ala-Leu-^ (SEQ ID NO:118)

**Name:** EST87  
**Species:** geographus  
**Cloned:** Yes

**DNA Sequence:**

CGGGCGCTGCATTCCGGACGTGAAACAGCATCGCCAGCAAGTGGGCATAGTGCAAG  
 ACACICAGAACAAGACGCACATAGTCTGANAAAAATAACCATGGGTATGCGGATGAN  
 GTTTAGTGTGTTTCNCGAGGTTGTCNTGGGNACCACTGTCGTTTCCTTCACNTCACGT  
 CGTGGTCCAAAAATCTCGTCGCGGGGAACCTATTCGACCACCTGTAATCAACTACGG  
 GGAGTGTGTGAAGTATCCATCCTGTTGGGTTAAGGTGAAGGATTCCAGTGTCTGG  
 AGCAAGTCTCTCCAACTGAACCACGACATGTCGCCTCTGCCTGACCTGCTTCACGT  
 TCCGTCTCTTCTGCCACTAGAACTCAACAACCTCGATCCAACAGACTCCTACTTTAC  
 CTCCGTATTCTGAAACTACTTGGATTGATTGTCTTTAATATCTACTCACACTTGCTG  
 TTATTACATCATCCAAAAATTAACAAGAACATGAAAGGTGCTGTTCAAACAAAATC  
 AGGCAATGACAANGGGGGAAAGTCTCCANTCTATCTGAAAACCTGTCACCTGTCACT  
 CTCTTAACCAAGGTTTANAACCTGANTACCACTANAGCTGTTGTNCCACATCANGATCA  
 GNCCAAATTTGTANNGTTCCTTTGCAAAACCTTTGCCTGAAATTCCTTGAAAAAGAAAC  
 GCTCACAATGTTGGGAAGTGCTTTNATTANCTGACAANNNTGNCANCATGTTCCNTT  
 TCANTAANTCTNAAATGNAAACCTCTGTT (SEQ ID NO:119)

**Translation:**

MGMRMMFVFLQVVLGTTVVFSSTRRGPKSRRGEPIPTTVINYGECKDPSCWVKVKD  
 FQCPGASPPN (SEQ ID NO:120)

**Toxin Sequence:**

Gly-Xaa1-Xaa3-Ile-Xaa3-Thr-Thr-Val-Ile-Asn-Xaa5-Gly-Xaa1-Cys-Cys-Lys-Asp-Xaa3-Ser-  
 Cys-Xaa4-Val-Lys-Val-Lys-Asp-Phe-Gln-Cys-Xaa3-Gly-Ala-Ser-Xaa3-Xaa3-Asn-^ (SEQ ID  
 NO:121)

**Name:** G12.1

**Species:** geographus

**Cloned:** Yes

**DNA Sequence:**

AGCCTTGATACAGAGCTGGTATCTGCTGTTAATACTTGAAAGAACAAGTGCTGTGA  
 GCCTTCATCTCTCTCTGACTTTAGTTTGGGTCCTGGAGAAAACCTTGACGGGCAGTA  
 TGAAAATTTACCTGTGTCTTGCTTTGTTCTGCTCCTGGCTTCTACCATAGTTGATTC  
 AGGGCTTCTTGATAAAATTGAGACTATAAGAACTGGAACGCGATGACAGCTATT  
 GTGATGGATGCCTATGCACCATATTAAGAGAGACTTGCACATCGACTATGAGC  
 TGCAGGGGAACATGCCGAAAAGAGTGGCCATGTTGGGAAGAAGACTGCTACTGTAC  
 TGAATCCAAGGTGGAGCTTGCCTCACACCCCTCAGAATGCAAACCTGGAGAGTGTT  
 GAGGATTGGAGTGGCCAGTTCAGCACATACAGCACCATGGTGCCCTGGACAATCG  
 TCTATTGAATTGAATATGCCTGTGGCAGGAATCTGTCTACAAAATAAAAAATCAT  
 AAGTTAAAAAA (SEQ ID NO:122)

**Translation:**

MKIYLCLAFVLLLASTIVDSGLLDKIETIRNWKRDDSYCDGLCTLKKETCTSTMSCRG  
 TCRKEWPCWEEDCYCTEIQGGACVTPSECKPGE (SEQ ID NO:123)

**Toxin Sequence:**

Asp-Asp-Ser-Xaa5-Cys-Asp-Gly-Cys-Leu-Cys-Thr-Ile-Leu-Lys-Lys-Xaa1-Thr-Cys-Thr-Ser-  
 Thr-Met-Ser-Cys-Arg-Gly-Thr-Cys-Arg-Lys-Xaa1-Xaa4-Xaa3-Cys-Xaa4-Xaa1-Xaa1-Asp-Cys-  
 Xaa5-Cys-Thr-Xaa1-Ile-Gln-Gly-Gly-Ala-Cys-Val-Thr-Xaa3-Ser-Xaa1-Cys-Lys-Xaa3-Gly-  
 Xaa1-Cys-^ (SEQ ID NO:124)

**Name:** G12.2

**Species:** geographus

**Cloned:** Yes

**DNA Sequence:**

AACGTTGACGGGCAGTATGAACATTTACCTGTGTCTTGCTTTTCTTCTGTTCCTGCCT  
 TCTACCATAGTTGATTCAGGGCTTCTTGATAAAATTGAGACAATAAGGAATTGGAGA  
 CGTGATGAAAGCAAGTGTGATCGATGCAATTGCGCGGAATTAGATCATCCAGATG  
 CACACAAGCTATCTTCTGCCTTACACCGGAGTTATGCACACCGAGCATCTCATGTCC

GACAGGTGAATGCCGCTGTACTAAGTTCCATCAGTCAAGATGCACTAGATTCGTAG  
AATGCGTACCTAATAAGTGTAGAGACGCATAGAGGCCAGTTCACGCACATACAGCA  
CCATGATGCCCTGGACAATCGTGTTGTTGGATTGAATATGCCCGTGGCAGGAATCTG  
TCCTACAAAAAA (SEQ ID NO:125)

# **Translation:**

MNIYLCLAFLLFLPSTIVDSGLLDKIETIRNWRRDESKCDRCNCAELRSSRCTQAIFCLTP  
ELCTPSISICTPGEICRCKFKHQSRCTRFVECVPNKCRDA (SEQ ID NO:126)

# **Toxin Sequence:**

Asp-Xaa1-Ser-Lys-Cys-Asp-Arg-Cys-Asn-Cys-Ala-Xaa1-Leu-Arg-Ser-Ser-Arg-Cys-Thr-Gln-  
Ala-Ile-Phe-Cys-Leu-Thr-Xaa3-Xaa1-Leu-Cys-Thr-Xaa3-Ser-Ile-Ser-Cys-Xaa3-Thr-Gly-Xaa1-  
Cys-Arg-Cys-Thr-Lys-Phe-His-Gln-Ser-Arg-Cys-Thr-Arg-Phe-Val-Xaa1-Cys-Val-Xaa3-Asn-  
Lys-Cys-Arg-Asp-Ala-^ (SEQ ID NO:127)

**Name:** Scratching,convulsion  
**Species:** geographus  
**Isolated:** Yes

# **Toxin Sequence:**

Lys-Phe-Leu-Ser-Gly-Gly-Phe-Lys-Xaa1-Ile-Val-Cys-His-Arg-Xaa5-Cys-Ala-Lys-Gly-Ile-Ala-  
Lys-Xaa1-Phe-Cys-Asn-Cys-Xaa3-Asp-# (SEQ ID NO:128)

**Name:** Contryphan-Im  
**Species:** imperialis  
**Isolated:** Yes

# **Toxin Sequence:**

Xaa2-Cys-Gly-Gln-Ala-Xaa4-Cys-# (SEQ ID NO:129)

**Name:** Im9.1  
**Species:** imperialis  
**Cloned:** Yes

# **DNA Sequence:**

GTAAAAATGCATCTGTCACTGGCAAGCTCAGTGCTTTGATGTTGCTTCTGCTTTTTG  
CCTTGGGCAACTTCGTTGGGGTCCAGCCAGGACAAATAAGAGATCTGAACAAAGGA  
CAGCTCAAGGACAACCGCCGTAACCTGCAATCGCAGAGGAAACAAATGAGTCTCCT  
CAAGTCACTTCATGATCGAAATGGGTGTAACGGCAACAGTGTTCGAATAGCCCT  
GCCCTAACAACTGTTATTGCGATACTGAGGACGACTGCCACCCTGACAGGCGTGAA  
CATTAGAGATTAGAGAGTTTCCTTGTCACATGATGTCGCACCACACCTCTGCTCTG  
CAGTGTGTACATCGACACAGTCGACGCATCTGTTATTTCTTTGTCGTGTGGATTGTACA  
TCGACCAGTCCACGCATCTGTTATTTCTTTGTCTGTTGATTGTTTTCGTGTGTTTCAT

AACACACAGAGCCTTTCTATTATCTGTATTGCAATACACTTTGCCTGATAACCAGAA  
AGTCCAGTGCT (SEQ ID NO:130)

#### Translation:

MHL<sup>5</sup>SLASSAALMLLLL<sup>10</sup>FALGNFVGVQPGQIRDLNKGQLKDNRRNLQSQRKQMSLLKSL  
HDRNGCNGNTCSNSPCPN<sup>15</sup>NCYCDTEDDCHPDRREH (SEQ ID NO:131)

#### Toxin Sequence:

Asn-Gly-Cys-Asn-Gly-Asn-Thr-Cys-Ser-Asn-Ser-Xaa3-Cys-Xaa3-Asn-Asn-Cys-Xaa5-Cys-  
10 Asp-Thr-Xaa1-Asp-Asp-Cys-His-Xaa3-Asp-Arg-Arg-Xaa1-His-<sup>^</sup> (SEQ ID NO:132)

**Name:** La8.1  
**Species:** laterculatus  
**Cloned:** Yes

#### DNA Sequence:

ATGATGTCGAAAATGGGAGCTATGTTTGTCTTTGCTTCTTTTCACCTGGCATCCA  
GCCAGCAGGAAGGAGATGTCCAGGCAAGGAAAAACACACCCGAAGAGAGAGTTCCA  
TCGTATTCTGCTAAGGCCTGACAGACAGTCCGAAACGGCTTGTAGGTCGCTCGGAA  
GCTACCAATGTATGGGTAATGCCAACTCGGGGTTCATTCTGGTGTGAATGCATT  
ATAACCGAGGTAGTCAGAAGTCTGGATGCGCGTGTAGGTGTCAAAAGTGATTAATT  
GACTCATTTAACTCGTTGAACGATTTAAAAAATCCAGAGCAATATGTTTCGAGAAAA  
ACCGAAGACGAC (SEQ ID NO:133)

#### Translation:

MMSKMGAMFVLLLLFTLASSQ<sup>5</sup>QEGDVQARKTHPKREFHRI<sup>10</sup>LLRPDRQSETACRSLGSY  
QCMGK<sup>15</sup>CQLGVH<sup>20</sup>SWCEIYN<sup>25</sup>NRGSQKSGCACRCQK (SEQ ID NO:134)

#### Toxin Sequence:

Xaa2-Ser-Xaa1-Thr-Ala-Cys-Arg-Ser-Leu-Gly-Ser-Xaa5-Gln-Cys-Met-Gly-Lys-Cys-Gln-Leu-  
Gly-Val-His-Ser-Xaa4-Cys-Xaa1-Cys-Ile-Xaa5-Asn-Arg-Gly-Ser-Gln-Lys-Ser-Gly-Cys-Ala-  
Cys-Arg-Cys-Gln-Lys-<sup>^</sup> (SEQ ID NO:135)

**Name:** Lv6.2  
**Species:** lividus  
**Cloned:** Yes

#### DNA Sequence:

GGATCCATGAAACTGACGTGTGTGGTGATCATCGCCGTGCTGTTCTGACGGCCAGT  
CAGCTCATTACAGCTGATTACTCCAGAGATAAGCAGGAGTATCGTGCAGAGAGGCT  
GAGAGACGCAATGGGGA<sup>5</sup>AAATCAAAGGTTCCAGGTCTGTCGGACATAGTGGTGCAG  
GTTGTTATACTCGCCCTTGTGCCCTGGTCTGCATTGCTCTGGCGGCCAAGCTGGAG  
GCCTGTGCGTGTAAATAGTAATAATCTGGCGTCTGATATTTCCAGTCTGTGCTTACC  
CTCTTTTGCTGAGTCATCCATACCTGTGCTCGAG (SEQ ID NO:136)

**Translation:**

MKLTCVVIIAVLFLTASQLITADYSRDKQEYRAERLRDAMGKFKGSRSCGHSGAGCYT  
 RPCCPLHCSGGQAGGLCV (SEQ ID NO:137)

**Toxin Sequence:**

Ser-Cys-Gly-His-Ser-Gly-Ala-Gly-Cys-Xaa5-Thr-Arg-Xaa3-Cys-Cys-Xaa3-Gly-Leu-His-Cys-  
 Ser-Gly-Gly-Gln-Ala-Gly-Gly-Leu-Cys-Val-^ (SEQ ID NO:138)

**Name:** Lv6.3  
**Species:** lividus  
**Cloned:** Yes

**DNA Sequence:**

GGATCCATGAAACTGACGTGTGTGGTGATCATATCCGTGCTGTTCTCTGACGGCCAGT  
 GAGTTCCCTACAGCTGATTACTCCAGAGATAAGCGGCAGTACCGTGCTGTGAGGTTG  
 AGAGACGCAATGCGGAATTTCAAAGGTACCAGGGACTGCGGGGAATCAGGTCAAG  
 GTTGCTATAGTGTACGTCCTTGCTGCCCTGGTCTGATTGTGCAAAGGCACCGGTGGT  
 GAGGCCTGTGCCGGCCCTCTGGCATCTGATATCTCCCTCTGTGCTCCACCCTCTTTT  
 GCCTGAGTCATCCATACCTGTGCTCGAG (SEQ ID NO:139)

**Translation:**

MKLTCVVIIIVLFLTASEFLTADYSRDKRQYRAVRLRDAMRNFKGTRDCGESGQGCYS  
 VRPCCPLICKGTGGGGLCRPSGI (SEQ ID NO:140)

**Toxin Sequence:**

Asp-Cys-Gly-Xaa1-Ser-Gly-Gln-Gly-Cys-Xaa5-Ser-Val-Arg-Xaa3-Cys-Cys-Xaa3-Gly-Leu-Ile-  
 Cys-Lys-Gly-Thr-Gly-Gly-Gly-Gly-Leu-Cys-Arg-Xaa3-Ser-Gly-Ile-^ (SEQ ID NO:141)

**Name:** Convulsant  
**Species:** magus  
**Isolated:** Yes

**Toxin Sequence:**

Val-Xaa5-Xaa1-Thr-His-Xaa3-^ (SEQ ID NO:142)

**Name:** MAG-1  
**Species:** magus  
**Isolated:** Yes

**Toxin Sequence:**

Arg-Xaa3-Lys-Asn-Ser-Xaa4-^ (SEQ ID NO:143)

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**Name:** MAG-2  
**Species:** magus  
**Isolated:** Yes

5 **Toxin Sequence:**  
 Ala-Arg-Xaa3-Lys-Asn-Ser-Xaa4-? (SEQ ID NO:144)

**Name:** MAG-3  
**Species:** magus  
**Isolated:** Yes

**Toxin Sequence:**

Arg-Xaa3-Lys-Asn-Ser-Xaa4-^ (SEQ ID NO:145)

**Name:** Mi6.2  
**Species:** miles  
**Cloned:** Yes

**DNA Sequence:**

GGATCCATGAAACTGACGTGCGTGGTGATCGTCGCCGTGCTGTTCTCTGACGGCCTGT  
 CAACTCATTACTGCTGCGAATTACGCCAGAGATGAACAGGAGTACCCCGCTGTGAG  
 GTCGAGCGACGTGATGCAGGATTCCGAAGACTTGACGTTGACCAAGAAATGCACGG  
 ACGATTCTCAGTTCTGTAACCCTTCGAATCATGACTGCTGCAGTGGGAAGTGTATCG  
 ACGAAGGAGACAACGGCATATGCGCTATAGTCCCTGAAAACCTCTTAACAATGTATA  
 CTGACATTTCCCCCTCTGTGCTCCGCCGTCCGTGGCCTGACTCGTCCATCCTTGGGCG  
 TGGTCATGAACCGCTCGGTT (SEQ ID NO:146)

**Translation:**

MKLTCCVIVAVLFLTACQLITAANYARDEQEYPAVRSSDVMQDSEDLTLTKKCTDDSQ  
 FCNPSNHDCSGKCIDEGDNGICAIVPENS (SEQ ID NO:147)

**Toxin Sequence:**  
 Cys-Thr-Asp-Asp-Ser-Gln-Phe-Cys-Asn-Xaa3-Ser-Asn-His-Asp-Cys-Cys-Ser-Gly-Lys-Cys-Ile-  
 Asp-Xaa1-Gly-Asp-Asn-Gly-Ile-Cys-Ala-Ile-Val-Xaa3-Xaa1-Asn-Ser-^ (SEQ ID NO:148)

**Name:** Mi6.3  
**Species:** miles  
**Cloned:** Yes

**DNA Sequence:**

GGATCCATGAAACTGACGTGTGTGGTGATCGTCGCCGTGCTGTTCTCTGACGGCCTGT  
 CAACTCATTACTGCTGCGAATTACGCCAGAGATGAACAGGAGTACCTGCTGTGAG  
 GTCGAGCGACGTGATGCAGGATTCCGAAGACCTGACGTTGACCAAGAAATGCACGG

AGGATTCTCAGTTCTGTAACCCCTTCGAATCATGACTGCTGCAGTGGGAAGTGTATCG  
ACGAAGGAGACAACGGCATATGCGCTATAGTCCCTGAAAACCTTAACAATGTATA  
CTGACATTTCCCTCTGTGCTCCGCCGTCCGTGGCCTGACTCGTCCATCCTTGGGCG  
TGGTCATGAACCGCTCG (SEQ ID NO:149)

**Translation:**

MKLTCVVIVAVLFLTACQLITAANYARDEQEYPAVRSSDVMQDSEDLTLTKKCTEDSQ  
FCNPSNHDCCSGKCIDEGDNGICAIVPENS (SEQ ID NO:150)

**Toxin Sequence:**

Cys-Thr-Xaa1-Asp-Ser-Gln-Phe-Cys-Asn-Xaa3-Ser-Asn-His-Asp-Cys-Cys-Ser-Gly-Lys-Cys-  
Ile-Asp-Xaa1-Gly-Asp-Asn-Gly-Ile-Cys-Ala-Ile-Val-Xaa3-Xaa1-Asn-Ser-^ (SEQ ID NO:151)

**Name:** Mf6.1  
**Species:** miliaris  
**Cloned:** Yes

**DNA Sequence:**

GGATCCATGAACTGACGTGTGTGGTGATCATCGCCGTGCTGTTCCCTGACGGCCTGTC  
AACTCACTACAGCTGTGACTTCTCCAGAGGTCAACAGAAGCATCGTGCTCTGAGGT  
CAACTGACAAAAACTCCAGGATGACCAAGCGTTGCACGCCTCCAGGTGGACTCTGT  
TACCATGCTTATCCCTGCTGCAGCAAGACTTGAATCTCGATACCAGCCAATGTGAG  
CCTAGGTGGTCATGAACCACTCAATACCCCTCTCCTCTGGAGGCTTCAGAGGAACTAC  
ATTGAAATAAAACCGCATTGCAACGAAAAAAAAAAAAAAAAAAAA (SEQ ID NO:152)

**Translation:**

LTCVVIIAVLFLTACQLTTAVTSSRGQQKHLRLRSTDKNSRMTKRCTPPGGLCYHAYPC  
CSKTCNLDTSQCEPRWS (SEQ ID NO:153)

**Toxin Sequence:**

Cys-Thr-Xaa3-Xaa3-Gly-Gly-Leu-Cys-Xaa5-His-Ala-Xaa5-Xaa3-Cys-Cys-Ser-Lys-Thr-Cys-  
Asn-Leu-Asp-Thr-Ser-Gln-Cys-Xaa1-Xaa3-Arg-Xaa4-Ser-^ (SEQ ID NO:154)

**Name:** Mn10.3  
**Species:** monachus  
**Cloned:** Yes

**DNA Sequence:**

tgtgtgtgtgtgttctgggtccaGCATCTGATGTCAGGAATGCCGCAGTCCACGAAAGACAGAAG  
GATCTGGTTCGTTACGGCCACCACGACTTGCTGTGGTTATAATCCGATGACAATGTGC  
CCTCCTTGCATGTGCACTAATACCTGCAAAAAAAGTGGCTGATGCTCCAGGACCCTC  
TGAACCACGACGT (SEQ ID NO:155)

**Translation:**

SDVRNAAVHERQKDLVVTATTTCCGYNPMTMCPPCMCTNTCKKSG (SEQ ID NO:156)

**Toxin Sequence:**

Xaa2-Lys-Asp-Leu-Val-Val-Thr-Ala-Thr-Thr-Thr-Cys-Cys-Gly-Xaa5-Asn-Xaa3-Met-Thr-Met-Cys-Xaa3-Xaa3-Cys-Met-Cys-Thr-Asn-Thr-Cys-Lys-Lys-Ser-# (SEQ ID NO:157)

**Name:** Mn8.1  
**Species:** monachus  
**Cloned:** Yes

**DNA Sequence:**

ATGATGTCGAAAAATGGGAGCTATGTTTGTCTTTTGCTTCTTTTCACCCTGGCATCCA  
GCCAGCAGGAAGGAGATGTCCAGGCAAGGAAAACAAGCCTGAAGAGCGACTTCTA  
TCGTGCTCTGAGAGGGTATGACAGACAGTGCACCTTTGTCAACAATTGTGACCGGA  
ACGGTGAGCGTGCCTGTAAACGGTGATTGCTCTTGCAGGGCCAGATTGTAAATGC  
GGTTATAGAGTCAGTCCTGGGAAGTCAGGATGCGCGTGTACTTGTAGAAATGCCAA  
ATGAATCATTTAACTCGTTGAAAAGATTTTTAAAAATCCAGAGCTATATGTTTCGAGA  
AAAACCGAAGAC (SEQ ID NO:158)

**Translation:**

MMSKMGAMFVLLLLFTLASSQEGDVQARKTSLKSDFYRALRGYDRQCTLVNNCDRN  
GERACNGDCSECGICKGYRVSPGKSGCACTCRNAK (SEQ ID NO:159)

**Toxin Sequence:**

Xaa2-Cys-Thr-Leu-Val-Asn-Asn-Cys-Asp-Arg-Asn-Gly-Xaa1-Arg-Ala-Cys-Asn-Gly-Asp-Cys-  
Ser-Cys-Xaa1-Gly-Gln-Ile-Cys-Lys-Cys-Gly-Xaa5-Arg-Val-Ser-Xaa3-Gly-Lys-Ser-Gly-Cys-  
Ala-Cys-Thr-Cys-Arg-Asn-Ala-Lys-^ (SEQ ID NO:160)

**Name:** Pn1.3  
**Species:** pennaceus  
**Cloned:** Yes

**DNA Sequence:**

ATGCGCTGTCTCCAGTCTTCGTCTATTCTTCTGCTGCTGACTGCATCTGCACCTAGCG  
TTGATGCCAAAGTTTCATCTGAAGACCAAAGGTGATGGGCCCTGTCTATCTTCCGAG  
ATAATGCAAAGAGTACCCTACAAAGACTTCAGGACAAAAGCACTTGCTGTGGCTTT  
AAGATGTGTATTCCTGTGCTTAACCAAGCATGAAGGATCC (SEQ ID NO:161)

**Translation:**

MRCLPVFVILLLLTASAPSVDAKVHLKTKGDGPLSSFRDPAKSTLQRLQDKSTCCGFKM  
CIPCR (SEQ ID NO:162)

**Toxin Sequence:**

Ser-Thr-Cys-Cys-Gly-Phe-Lys-Met-Cys-Ile-Xaa3-Cys-Arg-^ (SEQ ID NO:163)

**Name:** Pn9.1  
**Species:** pennaceus  
**Cloned:** Yes

**DNA Sequence:**

ATGTTGCTTCTGCTGTTTGCCTTGGGCAGCTTCGTTGTGGTCCAGTCAGGACAGATA  
ACAAGAGATGTGGACAATGGGCAGCTCGCGGACAACCGCGTACCCTGCCATCGCA  
GTGGAAGCAAGTGAGTTTCTTCAAGTCACTTGATAAACGACTGACTTGTAACGATCC  
TTGCCAGATGCATTCCGATTGCGGCATATGTGAATGCGTGAAAAATAAATGCATATT  
TTTCATGTAAACGGATTGAGTTTGCTTGTC AACACAATGTGCGACTGCAGCTCTTCT  
CTACCGGTGGGTACATCGACCAAACGACGCATCTTTATTCTTTGTCTGTTTCGTTT  
GTTCTCCTGTGTTCATAACGTACAGAGCCCTTAACTACCCTTACTGCTCTTCACTTA  
ACCTGATAACCTGAAGGTCCGGTGCAGCTGGCGTAGCCTTCACAGTTTCG (SEQ ID  
NO:164)

**Translation:**

MLLLLFALGSFVVVQSGQITRDVDNGQLADNRRLRSQWKQVSFFKSLDKRLTCNDPC  
QMHSDCGICECVENKCIFFM (SEQ ID NO:165)

**Toxin Sequence:**

Leu-Thr-Cys-Asn-Asp-Xaa3-Cys-Gln-Met-His-Ser-Asp-Cys-Gly-Ile-Cys-Xaa1-Cys-Val-Xaa1-  
Asn-Lys-Cys-Ile-Phe-Phe-Met-^ (SEQ ID NO:166)

**Name:** Pu6.1  
**Species:** pulicarius  
**Cloned:** Yes

**DNA Sequence:**

ATGAAACTGACGTGTGTGGTGATCGTCGCCGTGCTGTTTCCTGACGGCCTGTCAACTC  
AGTACAGCTGATGACTCCAGAGATGAGCAGCAGGATCCTTTGGTGAGGTCGCATCG  
TGAGGAGCAGAAAAGCCGAGGACCCCAAGACGGCCGAGAGATGTTCAGATTTCCGA  
TCCGACTGTGTTCTGCTACTCATAACTGCTGCAGTGGTGAATGTTTGGCTTCGAG  
GACTTCGGCTTATGCACGTAAAACTGGTCTGACGTCTGATATCCCCCTCTGTCTT  
CATCCTCTTTTGCCTGATTCCATCCATACCTATATGCTCCTGAACCGCTGTGTACCT  
TTACCCCTGGTGGCTTCAGAGGACGTTATATCAAAATAAAACCGCGTTGCAATGACA  
AAAAAAAAAAAAAAAAAAAA (SEQ ID NO:167)

**Translation:**

MKLTCVVIVAVLFLTACQLSTADDSRDEQQDPLVRSHREEQKAEDPKTAERCSDFGSD  
CVPATHNCCSGECFGFEDFGLCT (SEQ ID NO:168)

**Toxin Sequence:**

Cys-Ser-Asp-Phe-Gly-Ser-Asp-Cys-Val-Xaa3-Ala-Thr-His-Asn-Cys-Cys-Ser-Gly-Xaa1-Cys-  
Phe-Gly-Phe-Xaa1-Asp-Phe-Gly-Leu-Cys-Thr-^ (SEQ ID NO:169)

**Name:** Bromosleeper-P1  
**Species:** purpurascens  
**Cloned:** Yes

#### DNA Sequence:

GACAGGATTGAACAAATTCAGGATGTCAAGATTGGAATCATGGTGCTAACCTTT  
 CTACTTCTTGTGTCCATGGCAACCAAGCCATCGTTATGCAAGAGGGAAGCAGGCGAC  
 GCGAAGGAACGCAATCAACATCAGACGGAGAAGCACACCAAAAACTGAGGCGTGC  
 GAAGAGGTCTGTGAGCTGGAAGAAAAGCACTGCTGCTGCATAAGAAAGTGACGGAC  
 CCAATGTGCCGTAAGTGCCTGTTGTCAATCTTCTGTTAGTTTCTGTACACTGTCTC  
 ATTCATTATCTTATCAGTACAAGTGTAAACGAGACATGTCAGAAAGTCGAAGGTTGT  
 GCGTAATTTGATAAGTATTGTTGCTGGGATGAACGGA (SEQ ID NO:170)

#### Translation:

MSRFGIMVLTFLLVSMATSHRYARGKQATRRNAINIRRRSTPKTEACEEVCELEEKHC  
 CCIRSDGPKCSRKCLLSIFC (SEQ ID NO:171)

#### Toxin Sequence:

Xaa3-Lys-Thr-Xaa1-Ala-Cys-Xaa1-Xaa1-Val-Cys-Xaa1-Leu-Xaa1-Xaa1-Lys-His-Cys-Cys-  
 Cys-Ile-Arg-Ser-Asp-Gly-Xaa3-Lys-Cys-Ser-Arg-Lys-Cys-Leu-Leu-Ser-Ile-Phe-Cys-^ (SEQ ID  
 NO:172)

**Name:** Bromosleeper-P2  
**Species:** purpurascens  
**Cloned:** Yes

#### DNA Sequence:

GACAGGATTGAACAAATTCAGGATGTCAGGATTGGGAATCATGGTGCTAACCTT  
 CTACTTCTTGTGTCCATGGCAACCAACCATCAGGATAGAGGAGAGAAGCAGGTGAC  
 GCGAAGGGACGCAATCAACGTCAGACGGAGAAGATCAATCAACCCAGCAAGTCGTA  
 TCTGAGGAGTGCAAAAAAGTACTGTGAAGAAACAGAAAGAAATGCTGCGACAGTAA  
 ACATGAAGAACCAGATGTGCCAAGATATGCTTCGGATAGTTTCTGTACACGGTCTC  
 ATTCATTATTTTATCAGTACAAGTAAACGAGACCTATCAGAAAGTCGAAGGTTGTGC  
 ATAATTTGATAAACATTGTTTGTCTGGGATGAACGGA (SEQ ID NO:173)

#### Translation:

MSGLGIMVLTLTLLVSMATNHQDRGEKQVTQRDAINVRRRRSITQVVSECKKYCKK  
 QNKNCCSSKHEEPRCAKICFG (SEQ ID NO:174)

#### Toxin Sequence:

Val-Val-Ser-Xaa1-Xaa1-Cys-Lys-Lys-Xaa5-Cys-Lys-Lys-Gln-Asn-Lys-Asn-Cys-Cys-Ser-Ser-  
 Lys-His-Xaa1-Xaa1-Xaa3-Arg-Cys-Ala-Lys-Ile-Cys-Phe-# (SEQ ID NO:175)

**Name:** P29  
**Species:** purpurascens

**Isolated:** Yes

**Toxin Sequence:**

Asp-Cys-Cys-Gly-Val-Lys-Leu-Xaa1-Met-Cys-His-Xaa3-Cys-Leu-Cys-Asp-Asn-Ser-Cys-Lys-Asn-Xaa5-Gly-Lys-# (SEQ ID NO:176)

**Name:** P4.1

**Species:** purpurascens

**Cloned:** Yes

**DNA Sequence:**

ATGTTCCACCGTGTTTCTGTGGTTGTCTTGGCAACCACTGTCGTTTCCTTCACTTCAG  
ATCGTGCAATCGGATGACAGGAATACCAACGACAAAGCATCTCGCCTGCTCTCTCAC  
GTTGTCCAGGGGATGCTGTGGTAGCTATCCCAATGCTGCCTGTCATCCTTGCGGTTGT  
AAAGATAGGCCATCGTATTGTGGTCAAGGACGCTGATGCTCCAGGACCTCTGAAC  
CACGACGT (SEQ ID NO:177)

**Translation:**

MFTVFLLVVLATTVVVSFTSDRASDDRNTNDKASRLLSHVVRGCCGSSYPNAACHPCGCK  
DRPSYCGQGR (SEQ ID NO:178)

**Toxin Sequence:**

Gly-Cys-Cys-Gly-Ser-Xaa5-Xaa3-Asn-Ala-Ala-Cys-His-Xaa3-Cys-Gly-Cys-Lys-Asp-Arg-Xaa3-Ser-Xaa5-Cys-Gly-Gln-# (SEQ ID NO:179)

**Name:** P4.2

**Species:** purpurascens

**Cloned:** Yes

**DNA Sequence:**

ATGTTCCACCGTGTTTCTGTGGTTGTCTTGGCAACCACTGTCGTTTCCTTCAACGTAG  
ATCGTGCAACTGATGGCAGGAGTGCTGCAGCCATAGCGTTTGCCCTGATCGCTCCGA  
CCGTCCGGGAAGGATGCTGTTCTAATCCTGCCTGTCATCCTTGCGGTTGTAAAGATA  
GGCCATCGTATTGTGGTCAAGGACGCTGATGCTCCAGGACCTCTGAACCACGACG  
T (SEQ ID NO:180)

**Translation:**

MFTVFLLVVLATTVVVSFTVDRATDGRSAAAIAFALIAPTVREGCCSNPACHPCGCKDRP  
SYCGQGR (SEQ ID NO:181)

**Toxin Sequence:**

Xaa1-Gly-Cys-Cys-Ser-Asn-Xaa3-Ala-Cys-His-Xaa3-Cys-Gly-Cys-Lys-Asp-Arg-Xaa3-Ser-Xaa5-Cys-Gly-Gln-# (SEQ ID NO:182)

**Name:** P8.1  
**Species:** purpurascens  
**Cloned:** Yes

**DNA Sequence:**

ATGATGTCGAAAATGGGAGCTATGTTTGTCTTTTGTCTTCTTTTACCCTGGCATCCA  
 GCCAGCAGGAAAGGAGATGTCCAGGCAAGGAAAAACACGCCTGACGAGGGACTTCTA  
 TCGTACTCTGCCAGTGTCTACTAGAGGATGCAGCGGCTCCCCTTGTTTTAAAAACAA  
 AACGTGTCCGGATGAATGCATATGCGGCGGCTTATCCAATTGTTGGTGTGGCTACGG  
 CGGTAGTCGAGGATGCAAGTGTACATGTAGAGAGTGATTAATCGACTCTTAACTC  
 GTTGAATTATTTAAAAAATCCAGAGCAATATGTTTCGAGAAAAACCGAAGAC (SEQ ID  
 NO:183)

**Translation:**

MMSKMGAMFVLLLLFTLASSQEGDVQARKTRLTRDFYRILPVSTRGCSGSPCFKNKT  
 CRDECICGGLSNWCWGYGGSRGCKCTCRE (SEQ ID NO:184)

**Toxin Sequence:**

Gly-Cys-Ser-Gly-Ser-Xaa3-Cys-Phe-Lys-Asn-Lys-Thr-Cys-Arg-Asp-Xaa1-Cys-Ile-Cys-Gly-  
 Gly-Leu-Ser-Asn-Cys-Xaa4-Cys-Gly-Xaa5-Gly-Gly-Ser-Arg-Gly-Cys-Lys-Cys-Thr-Cys-Arg-  
 Xaa1-^ (SEQ ID NO:185)

**Name:** U021 homolog  
**Species:** purpurascens  
**Cloned:** Yes

**DNA Sequence:**

CGACCTCAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGCCTTGTTGA  
 CCATCTGTCTGCTTCTGTTTCCCATTAAGTCTTCTGATGGATGGAGATCAACCTGC  
 AGACCGACCTGCAGAACGTATGGATTACGACATTTTCATCTGAGGTGCATCGTTTGCT  
 TGAAGAAGAGACACCCGCCCTGTTGCATGTACGGCAGATGCCGTCGATATCCCGGAT  
 GCTCTAGTGCTCTTGTGTGCCAGGGAGGATAACGTGTTGATGACCAACTTTGTTACA  
 CGGTACTCGTCAAGTGTCTACTGAATAAGTAAAACGATTGCAGT (SEQ ID NO:186)

**Translation:**

MMSKLGALLTICLLFPITALLMDGDQPADRPAPERMDYDISSEVHRLLERRHPPCCMYG  
 RCRRYPGCSSASCCQGG (SEQ ID NO:187)

**Toxin Sequence:**

His-Xaa3-Xaa3-Cys-Cys-Met-Xaa5-Gly-Arg-Cys-Arg-Arg-Xaa5-Xaa3-Gly-Cys-Ser-Ser-Ala-  
 Ser-Cys-Cys-Gln-Gly-# (SEQ ID NO:188)

**Name:**  $\psi$ -PIIIF  
**Species:** purpurascens

**Isolated:** Yes

**Toxin Sequence:**

5 Gly-Xaa3-Xaa3-Cys-Cys-Leu-Xaa5-Gly-Ser-Cys-Arg-Xaa3-Phe-Xaa3-Gly-Cys-Xaa5-Asn-Ala-Leu-Cys-Cys-Arg-Lys-# (SEQ ID NO:189)

**Name:** Qc6.4

10 **Species:** quercinus

**Cloned:** Yes

**DNA Sequence:**

GGATCCATGAAACTGACGTGCGTGGTGATCATCGCCGTGCTGTTTCTGACAGCCAGT  
CAGCTCGTTACAGCTGATTACACCAGAGATAAATGGCAATACCCTGCAGCGAGTTT  
GAGAGGCGGAATGTGGAATTTGAGAGATACCAGGGCGTGCTCGCAAGTAGGTGAA  
GCTTGTTTTCCTCAGAAACCTTGCTGCCCTGGATTCTTTGCAATCACATCGGAGGC  
ATGTGCCACCACTAGTAACAGTCTGGCATCTGATATTTCCCCTCTGCGCTCCACCCT  
CTTTTGGCTGATTACCTTACCTGTGTGTGGTCATGAACCACTCAGTAGCTACACCT  
CTGGTGGCTTCAGAGGACGTATATCAAAATAAAACCACATTGCAAAAAAAAAAAAAA  
AAAA (SEQ ID NO:190)

**Translation:**

MKLTCVVIIAVLFTASQLVTADYTRDKWQYPAASLRGGMWNLRDTRACSQVGEACF  
PQKPCCPGFLCNHIGGMCHH (SEQ ID NO:191)

**Toxin Sequence:**

Ala-Cys-Ser-Gln-Val-Gly-Xaa1-Ala-Cys-Phe-Xaa3-Gln-Lys-Xaa3-Cys-Cys-Xaa3-Gly-Phe-Leu-Cys-Asn-His-Ile-Gly-Gly-Met-Cys-His-His-^ (SEQ ID NO:192)

**Name:** QcII

**Species:** quercinus

**Isolated:** Yes

**Toxin Sequence:**

Asp-Cys-Gln-Xaa3-Cys-Gly-His-Asn-Val-Cys-Cys-^ (SEQ ID NO:193)

**Name:** EST171

**Species:** radiatus

**Cloned:** Yes

**DNA Sequence:**

CATGAACTGTCTCGTACTGGCTTTGGTTACCATCGGTCTTCTGGCTGCAACAACCGC  
AGCCCTCTGGACACCACCACGGTCCTCCTCAGCACAACTACACGGCATGTCAAGG  
GCTGTGTGTACGAGGGCATAGAGTACAGTGTGCGAGAGACCTACCAGGCAGACTGC

AACACGTGTCGCTGTGATGGCTTTGACCTGGCTACATGCACCGTCGCGGGCTGCACA  
GGCTTTGGACCCGAGTGATTGGTACTATTCCACACCTAGCAATGTTACACTGGAAC  
CGGAACTTGATACTACCTTCTAAATATAATCAATTTGTTTCAAAGGCCCAA (SEQ  
ID NO:194)

#### Translation:

MNCLVLALVTIGLLAATTAAPLDTTTLVLLSTTRDVKGCVEGIEYSVGETYQADCNTC  
RCDGFDLATCTVAGCTGFGE (SEQ ID NO:195)

#### Toxin Sequence:

Gly-Cys-Val-Xaa5-Xaa1-Gly-Ile-Xaa1-Xaa5-Ser-Val-Gly-Xaa1-Thr-Xaa5-Gln-Ala-Asp-Cys-  
Asn-Thr-Cys-Arg-Cys-Asp-Gly-Phe-Asp-Leu-Ala-Thr-Cys-Thr-Val-Ala-Gly-Cys-Thr-Gly-Phe-  
Gly-Xaa3-Xaa1-<sup>^</sup> (SEQ ID NO:196)

**Name:** EST202  
**Species:** radiatus  
**Cloned:** Yes

#### DNA Sequence:

GTGAGAGTCCAACAGCCCAAACCTTTCAACTCACTATGTGGCAGTTGCAGTTTTCAA  
CGTCTGGACAGGATTCAACAAAATTCAGGATGTCAGGATTGGGAATCATGGTGCTA  
ACCCTTCTACTTCTTGTGTCCATGGCAACCAAGTCGTCAGGATAGAGGAGTGGGACAG  
CTGATGCCACGCGTCTCGTTCAAAGCCTGCAAATCAAATTATGATTGCCCGGAGCGT  
TTCAAATGTCGAGTTACACCTGGAATGGATCCAGTGGATACTGTAAACGTTGTTGC  
TATCTTTATCGTTAGTGTAATACACAAAGTGACTCTGTTCATTCTCTCCATCATCTC  
TTTGAAACAACACGGTGTGAGATCGTTTCTTTGTGATGAAGAGTAGTATCACGGG  
CAGAGTTCACTAGAGATCTCAAATGAAAAACAAGATTATTTAGTAAGTTGGGAAA  
ATCTGGATCTCGAAAAGATTCTTGAAGAACTCCGTATTTAACACGCTTGAGAGATGA  
TAATAAAGAATTCTGAAAGACaAA (SEQ ID NO:197)

#### Translation:

MSGLGIMVLTLVSMATSRQDRGVQLMPRVSFKACKSNYDCPQRFKCCSYTWNG  
SSGYCKRVCYLYR (SEQ ID NO:198)

#### Toxin Sequence:

Ala-Cys-Lys-Ser-Asn-Xaa5-Asp-Cys-Xaa3-Gln-Arg-Phe-Lys-Cys-Cys-Ser-Xaa5-Thr-Xaa4-  
Asn-Gly-Ser-Ser-Gly-Xaa5-Cys-Lys-Arg-Val-Cys-Xaa5-Leu-Xaa5-Arg-<sup>^</sup> (SEQ ID NO:199)

**Name:** R8.1  
**Species:** radiatus  
**Cloned:** Yes

#### DNA Sequence:

ATGATGTCGAAAAATGGGAGCTATGTTGTCTTTTGCTTCTTTTACCCTGGCATCCA  
GCCAGCAGGAAGGAGATGTCCAGGCAAGGAAAAACACCCGAAGAGAGAGTTCCA

ACGTATTCTGCTAAGGTCTGGCAGAAAGTGCAATTTTCGACAAATGTAAGGTACCG  
 GAGTCTACAATTGTGGGGAATCCTGCTCATGCGAAGGTTTGACAGTTGTGCTGCA  
 CTTATAACATCGGTTCTATGAAGTCTGGATGCGCGTGTATTTGTACATACTATTAAT  
 GATTAATTGACTCGTTAACTCGTTGAACGATTTAAAAAATCCAGAGCAATATGTTCT  
 GAGAAAAACCGAAGAC (SEQ ID NO:200)

#### Translation:

MMSKMGAMFVLLLLFTLASSQQEGDVQARKTHPKREFQRILLRSGRKNFDKCKGTG  
 VYNGESCSEGLHSCRCTYNIGSMKSGCACICTYY (SEQ ID NO:201)

#### Toxin Sequence:

Lys-Cys-Asn-Phe-Asp-Lys-Cys-Lys-Gly-Thr-Gly-Val-Xaa5-Asn-Cys-Gly-Xaa1-Ser-Cys-Ser-  
 Cys-Xaa1-Gly-Leu-His-Ser-Cys-Arg-Cys-Thr-Xaa5-Asn-Ile-Gly-Ser-Met-Lys-Ser-Gly-Cys-  
 Ala-Cys-Ile-Cys-Thr-Xaa5-Xaa5-^ (SEQ ID NO:202)

**Name:** R8.2  
**Species:** radiatus  
**Cloned:** Yes

#### DNA Sequence:

ATGATGTCGAAAAATGGGAGCTATGTTTGTCTTTTGTCTTTTTCACCTGGCATCCA  
 GGCAGCAGGAAGGAGATGTCCAGGCAAGGAAAACACGCCTGACGAGCGACTTCTA  
 TAGTGTTCTGCAAAAGGTATGGACTAGGATGCGCTGGCACITGTGGITCAAGCAGCA  
 ATTGTGTTAGAGATTATGTGACTGCCCAAAACCCAATTGTTACTGCACCTGGCAAAAG  
 GCTTTTCGTCACCAGGATGCGGGGTGTTTCATGTTTGGGGTGATTAATTGGCTCTTTTA  
 ACTCGTTGAACGATTTAAAAAATCCAGAGCAATATGTTTCGAGAAAAACCGAAGAC  
 (SEQ ID NO:203)

#### Translation:

MMSKMGAMFVLLLLFTLASRQQEGDVQARKTRLTSDFYSVLQRYGLGCAGTCGSSSN  
 CVRDYCDCPKPNCYCTGKGFRQPGCGCSCLG (SEQ ID NO:204)

#### Toxin Sequence:

Xaa5-Gly-Leu-Gly-Cys-Ala-Gly-Thr-Cys-Gly-Ser-Ser-Ser-Asn-Cys-Val-Arg-Asp-Xaa5-Cys-  
 Asp-Cys-Xaa3-Lys-Xaa3-Asn-Cys-Xaa5-Cys-Thr-Gly-Lys-Gly-Phe-Arg-Gln-Xaa3-Gly-Cys-  
 Gly-Cys-Ser-Cys-Leu-# (SEQ ID NO:205)

**Name:** Bromosleeper-Sn  
**Species:** sponsalis  
**Cloned:** Yes

#### DNA Sequence:

GACAGGATTGAACAAAAATTCAGGATGTCAGGATTGGGAATCATGGTGCTGACCCCTT  
 TTGCTTCTTGTGTCCATGGCAACCAGCCATAAGGATGGAGGAGAGAAGCAGGCGAT  
 GCAAAGGGACGCAATCAACGTCAGACTGAGAAGATCACTCACTCGGAGAGCAGTA

ACTGAGGCGTGCACGGAGGACTGTAAGACTCAGGACAAGAAGTGCTGCGGCGAAA  
TGAATGGACAACACACATGTGCCAAGATATGCCTCGGATAGTCTCTGTACGCTGTCT  
CATTATTATCTCATCAGTACAAGTGTAACGAGACAGGTGAGAAAGTCGAAGGTT  
GTTTCGAAATTTGATAAGCATTGTTTACTGGGACGAACGGA (SEQ ID NO:206)

**Translation:**

MSGLGIMVLTLTLLVSMATSHKDGGEKQAMQRDAINVRLRRSLTTRAVTEACTEDCKT  
QDKKCCGEMNGQHTCAKICLG (SEQ ID NO:207)

**Toxin Sequence:**

Ala-Val-Thr-Xaa1-Ala-Cys-Thr-Xaa1-Asp-Cys-Lys-Thr-Gln-Asp-Lys-Lys-Cys-Cys-Gly-Xaa1-  
Met-Asn-Gly-Gln-His-Thr-Cys-Ala-Lys-Ile-Cys-Leu-# (SEQ ID NO:208)

**Name:** Contryphan-Sm-dW4, V7  
**Species:** *stercusmuscarum*  
**Isolated:** Yes

**Toxin Sequence:**

Gly-Cys-Xaa3-Xaa4-Gln-Xaa3-Val-Cys-# (SEQ ID NO:209)

**Name:** Conopressin-S  
**Species:** *striatus*  
**Isolated:** Yes

**Toxin Sequence:**

Cys-Ile-Ile-Arg-Asn-Cys-Xaa3-Arg-Gly-# (SEQ ID NO:210)

**Name:** S6.4  
**Species:** *striatus*  
**Cloned:** Yes

**DNA Sequence:**

AGGTCGACTCGTGCTTGCTGACGGAACGCTTGCCTTTTGTAGTAGGATCAGATGC  
TGCGGTACTTGCAATCAATCTTAAAGTCATGTGTGAGCTGATCCAGCGGTTGATCT  
TCTCCCTCTGTGCTCCATCCTTTTCTGCCTGAGTTCTCCTTACCTGAGAGTGGTCAT  
GAACCACTCATCACTACTCTTCTGGAGGCTTCAGAGGAGCTACAGTAAAATAAAA  
GCCGCATTGC (SEQ ID NO:211)

**Translation:**

STRCLPDGTSCLFSRIRCCGTCSSILKSCVS (SEQ ID NO:212)

**Toxin Sequence:**

Cys-Leu-Xaa3-Asp-Gly-Thr-Ser-Cys-Leu-Phe-Ser-Arg-Ile-Arg-Cys-Cys-Gly-Thr-Cys-Ser-Ser-Ile-Leu-Lys-Ser-Cys-Val-Ser-^ (SEQ ID NO:213)

5 **Name:** U010 homolog  
**Species:** striatus  
**Cloned:** Yes

#### DNA Sequence:

10 CGGCTTCTAATACGACTCACTATAGGGCAAGCAGTGGTAACAACGCAGAGTACGCG  
 GGGGGACGGCAGACCAGCTGGGGACCAGACAGACGTCAAACAGCATCGCAGTCAG  
 GTGTGGAGATCCCAAGACACCCAGAAGAAGGAGACAGAAGAGTTATCGTTCGTAAC  
 ACAATGGCCATGAACATGTCGATGACACTCTGCATGTTTGTAAATGGTCGTCGTGGCA  
 GCCACTGTCAATTGATTCCACTCAGTTACAAGAACCAGATCTCAGTCGCATGCGACGC  
 AGCGGGCCTGCTGACTGTTGCAGGATGAAAGAGTGTTGCACCGACAGAGTGAACGA  
 GTgTCTACAGCGCTATTCTGGCCGGGAAGATAAAATTCGTTTCGTTTGTATCAGGA  
 GGCCACAGTCACATGTGGATCTTTTAACGAAATCGTGGGCTGTTGCTATGGATATCA  
 AATGTGCATGATACGAGTTGTGAAACCGAACAGTCTAAGTGGGGCCATGAGGCGT  
 GCAAAACCCGTTTCTTGTGGTAACCCCTTGCGCTTGAGGTGTCCTCGCGCCACGTCACC  
 TGTGTACAGCGCGTCACAGAGCCCTGATCTTTATGCCCTTATCTGTCTTTTGTCTC  
 TTCTACTCTCTGAAGTCTTGAGGTTTGTTCATTCTGTCAATCATCTCACGCGCATC  
 CAAGTAAATAAAGGTGACGTGACAAAC (SEQ ID NO:214)

#### Translation:

MAMNMSMTLCMFVMVVVAATVIDSTQLQEPDLSRMRRSGPADCCRMKECCTDRVNE  
 CLQRYSGREDKFVSFCYQEATVTCGSFNEIVGCCYGYQMCMIRVVKPNLSGAHEACK  
 TVSCGNPCA (SEQ ID NO:215)

#### Toxin Sequence:

30 Ser-Gly-Xaa3-Ala-Asp-Cys-Cys-Arg-Met-Lys-Xaa1-Cys-Cys-Thr-Asp-Arg-Val-Asn-Xaa1-  
 Cys-Leu-Gln-Arg-Xaa5-Ser-Gly-Arg-Xaa1-Asp-Lys-Phe-Val-Ser-Phe-Cys-Xaa5-Gln-Xaa1-  
 Ala-Thr-Val-Thr-Cys-Gly-Ser-Phe-Asn-Xaa1-Ile-Val-Gly-Cys-Cys-Xaa5-Gly-Xaa5-Gln-Met-  
 Cys-Met-Ile-Arg-Val-Val-Lys-Xaa3-Asn-Ser-Leu-Ser-Gly-Ala-His-Xaa1-Ala-Cys-Lys-Thr-Val-  
 Ser-Cys-Gly-Asn-Xaa3-Cys-Ala-^ (SEQ ID NO:216)

35 **Name:** WG002  
**Species:** striatus  
**Isolated:** Yes

#### Toxin Sequence:

Xaa4-Ser-Xaa4-Arg-Met-Gly-Asn-Gly-Asp-Arg-Arg-Ser-Asp-Gln-^ (SEQ ID NO:217)

45 **Name:** Sx8.1  
**Species:** striolatus  
**Cloned:** Yes

10072602.021195

**DNA Sequence:**

ATGATGTCGAAAATGGGAGCTATGTTTGCCTTTTGCTTCTTTGACCCTGGCATCCA  
 GCCAGCAGGAGGGAGATGTCCAGGCAAGGAAAACAAGCCTGAAGAGCGACTTCTA  
 TCGTGCTCTGAGACCGTATGACAGACAGTGCACTTTGTCAACAATTGTCAACAGAA  
 CGGTGCGTGTAAACGGTGATTGCTCTTGCAGGGGACCAGATTGTAAATGCGGTTATAG  
 AATCAGTCCCTGGGAGGTGAGGATGCGCGTGTACTTGTAGAAATGCCAAATGAATCA  
 CTTAACTCGTTGAAAGATTTTTAAAAATCCAGAGCTATATGTTTCGAGAAAAACCGA  
 AGAC (SEQ ID NO:218)

**Translation:**

MMSKMGAMFVLLLLLTLASSQEGDVQARKTSLKSDFYRALRPYDRQCTFVNNCQQN  
 GACNGDCSCGDQICKCGYRISPRSGCACTCRNAK (SEQ ID NO:219)

**Toxin Sequence:**

Xaa2-Cys-Thr-Phe-Val-Asn-Asn-Cys-Gln-Gln-Asn-Gly-Ala-Cys-Asn-Gly-Asp-Cys-Ser-Cys-  
 Gly-Asp-Gln-Ile-Cys-Lys-Cys-Gly-Xaa5-Arg-Ile-Ser-Xaa3-Gly-Arg-Ser-Gly-Cys-Ala-Cys-Thr-  
 Cys-Arg-Asn-Ala-Lys-^ (SEQ ID NO:220)

**Name:** Ts6.3  
**Species:** tessulatus  
**Cloned:** Yes

**DNA Sequence:**

GGATCCATGAAACTGACGTGTGTGGTGATCATCGCCGTGCTGTTCTTGACGGCCTGT  
 CAATTCAATTATAGCTGATTTCTCCAGAGATAAGCGGGTACATCGTGCAGAGAGGTG  
 AGAGACATAATGCAGAATTCAGAGGTACAGGTGCGTGCAGGAAATTTGGTGAAGT  
 TTGTAGTTCTACCGCTTGCTGCCCTGATTTGGATTGCGTTGAGGCCTATTCACCCATC  
 TGTCTCTGGGAATAGTCTGGCATCTGATATTTCCCGTCTGTGCTCTACCTACTTCTGC  
 CGGATTCATCCATACCTATGTGTGGCCATGAACCACTCAGTACCTACACCTCTGGTG  
 GCTTCCTAGGGACGTATATCAAAATAAAACCACATTGCAAAAAAAAAAAAAAAAAAAAA  
 (SEQ ID NO:221)

**Translation:**

MKLTCVVIIVLFLTACQFIADFSDKRVRHRAERLRDIMQNFGRTRSCAEFGEVCSSTA  
 CCPDLDCVEAYSPICLWE (SEQ ID NO:222)

**Toxin Sequence:**

Ser-Cys-Ala-Xaa1-Phe-Gly-Xaa1-Val-Cys-Ser-Ser-Thr-Ala-Cys-Cys-Xaa3-Asp-Leu-Asp-Cys-  
 Val-Xaa1-Ala-Xaa5-Ser-Xaa3-Ile-Cys-Leu-Xaa4-Xaa1-^ (SEQ ID NO:223)

**Name:** 4/43 SNX  
**Species:** textile  
**Isolated:** Yes  
**Cloned:** Yes

10072602.021102

**DNA Sequence:**

CGATTGCAGGGGTTaCGATGCGCCGTGTAGCTCTGGCGCGCCATGTTGTGATTGGTG  
 GACATGTTTCAGCACGAACCAACCGCTGTTTTAGGCTGACCACAAGCCATCCGACAT  
 CACCACTCTCTCTCTCAGAGGCTTCAAGGCTTTTTGTCTCTCTTTGAAGAATCTTTA  
 CGAGTGAACAAACAAGTAGAATAGCACGTTTTTCCCCCTTTGAAAAATCAATAATG  
 GAGGTTAAACAAAACCTGTCTTCTCAATAAAGATTTATCATAAT (SEQ ID NO:224)

**Translation:**

IQGGGDERQKAKINFLSRSDRDCRGYDAPCSSGAPCCDWWTCSARTNRCF (SEQ ID NO:225)

**Toxin Sequence:**

Asp-Cys-Arg-Gly-Xaa5-Asp-Ala-Xaa3-Cys-Ser-Ser-Gly-Ala-Xaa3-Cys-Cys-Asp-Xaa4-Xaa4-  
 Thr-Cys-Ser-Ala-Arg-Thr-Asn-Arg-Cys-Phe-^ (SEQ ID NO:226)

**Name:** convulsion  
**Species:** textile  
**Isolated:** Yes

**Toxin Sequence:**

Asn-Cys-Xaa3-Xaa5-Cys-Val-Val-Xaa5-Cys-Cys-Xaa3-Xaa3-Ala-Xaa5-Cys-Xaa1-Ala-Ser-  
 Gly-Cys-Arg-Xaa3-Xaa3-# (SEQ ID NO:227)

**Name:** Tx1.6  
**Species:** textile  
**Cloned:** Yes

**DNA Sequence:**

ATGCACTGTCTCCCAATCTTCGTCATTCTTCTGCTGCTGACTGCATCTGGACCTAGCG  
 TTGATGCCCAACTGAAGACCAAAGATGATGTGCCCTGTCTCTTCCGAGATCATG  
 CAAAGAGTACCCTACGAAGACTTCAGGACAAACAGACTTGCTGTGGCTATAGGATG  
 TGTGTTCCTTGTGGTTAACGAGCATGAAGGATCC (SEQ ID NO:228)

**Translation:**

MHCLPIFVILLLLTASGPSVDAQLKTKDDVPLSSFRDHAKSTLRRQLQDKQTCCGYRMCV  
 PCG (SEQ ID NO:229)

**Toxin Sequence:**

Xaa2-Thr-Cys-Cys-Gly-Xaa5-Arg-Met-Cys-Val-Xaa3-Cys-# (SEQ ID NO:230)

**Name:** Tx6.14  
**Species:** textile  
**Cloned:** Yes

10072602;0224102

**DNA Sequence:**

GTTATGGAGCGATTGCTATAGTTGGTTAGGATCATGTATTGCGCCCTCGCAGTGTTG  
TTCTGAGGTTTGTGATTATTACTGCCGCTATGGCGATGAACTCGGACCACAAGCCA  
T (SEQ ID NO:231)

**Translation:**

LWSDCYSWLGSCIAPSQCSEVCDYYCRLWR (SEQ ID NO:232)

**Toxin Sequence:**

Asp-Cys-Xaa5-Ser-Xaa4-Leu-Gly-Ser-Cys-Ile-Ala-Xaa3-Ser-Gln-Cys-Cys-Ser-Xaa1-Val-Cys-  
Asp-Xaa5-Xaa5-Cys-Arg-Leu-Xaa4-Arg-^ (SEQ ID NO:233)

**Name:** Tx6.3  
**Species:** textile  
**Cloned:** Yes

**DNA Sequence:**

AGCTGACGAATGAAAAATCCGAGAATGTCAAGCTCAGCAAGAGAAAAATGTGTGGA  
ACAAATGGAAATACTGCACCCGAGAGTCCTTATGTTGCGCGGGTTTGTGTTTGTAG  
TTTCTGCATTCTATAACGCTAATCCAGAGTCGTATATCCGTCTAAGCTCCACCTGGC  
ACTGTCTGGTATGTTCTGCCAGTGACTGGTCTCATACCGCTTAGACTCTGGTCCGTC  
TTCTCTGCAACCACAGGAGAACGTGCATTATTACAATAAACGCATACTGC (SEQ ID  
NO:234)

**Translation:**

RMKNSENVKLSKRKCVEQWKYCTRESLCCAGLCLFSFCIL (SEQ ID NO:235)

**Toxin Sequence:**

Lys-Cys-Val-Xaa1-Gln-Xaa4-Lys-Xaa5-Cys-Thr-Arg-Xaa1-Ser-Leu-Cys-Cys-Ala-Gly-Leu-  
Cys-Leu-Phe-Ser-Phe-Cys-Ile-Leu-^ (SEQ ID NO:236)

**Name:** Tx6.7  
**Species:** textile  
**Cloned:** Yes

**DNA Sequence:**

CAGAGCCGCTCTGGTGTGCAGACCTGTCTCCAGCCCTCCGTCTCCCTGATCGGTGGT  
TCTGCCTGCATAGCTGTCTTCTCCACGAAGCTTTCCACAGGTATAAATAACGCTTCA  
GTCTCCCGTCCTGTATTGGGCCGCCGTTACAAGCCAGACCGATACAGCCAGGTCCA  
GTCTACTTTGCGAGTGAGTTAAAGCTCCAGCATTCTACCAGCATCACCAGAATGAA  
GGTGAGCAGCGCTGCTGATCGTGGCTACGCTGACACTGACCGCAGGCCAGCTGGTTA  
GTGCTTCTTCCATTACTCAAAAGATGTCCAGATTCTTCCTTCTGTGAGATCAGCTGA  
CGAAGTGGAAAAATCCGAGAATGTCAGGCTCAGCAAGAGAAGATGTGTGGAACAAAT

GGGAAGTCTGCGGCATAATCTTGTTCTCCTCATCATGTTGCGGGCAGTTGTGTTTGT  
TGGTTTCTGCGTTCTATAACGCTAATCCAGAGTCGTATATCCGCTCTAAGCTCCA  
(SEQ ID NO:237)

5 **Translation:**

MKVSSVLIVATLTLTAGQLVSASSHYSKDVQILPSVRSADENVRLSKRRRCVEQW  
EVCGILFSSSCCGQLCLFGFCVL (SEQ ID NO:238)

**Toxin Sequence:**

10 Cys-Val-Xaa1-Gln-Xaa4-Xaa1-Val-Cys-Gly-Ile-Ile-Leu-Phe-Ser-Ser-Ser-Cys-Gly-Gln-  
Leu-Cys-Leu-Phe-Gly-Phe-Cys-Val-Leu-^ (SEQ ID NO:239)

**Name:** TxVIIA

**Species:** textile

**Isolated:** Yes

**Toxin Sequence:**

Cys-Gly-Gly-Xaa5-Ser-Thr-Xaa5-Cys-Xaa1-Val-Asp-Ser-Xaa1-Cys-Cys-Ser-Asp-Asn-Cys-  
Val-Arg-Ser-Xaa5-Cys-Thr-Leu-Phe-# (SEQ ID NO:240)

**Name:** U030

**Species:** textile

**Isolated:** Yes

**Toxin Sequence:**

Gly-Cys-Asn-Asn-Ser-Cys-Gln-Xaa1-His-Ser-Asp-Cys-Xaa1-Ser-His-Cys-Ile-Cys-Thr-Ser-  
Arg-Gly-Cys-Gly-Ala-Val-Asn-# (SEQ ID NO:241)

**Name:** Bromosleeper-T1

**Species:** tulipa

**Cloned:** Yes

**DNA Sequence:**

CAGGATTGAACAAAAATTCAGGATGTCAGGATTGGAATCATGGTGCTAACCCCTTCT  
ACTTCTTGTTGCCATGGCAACCAGTCATCGTTATGCAAGAGAAAAAGCAGGCGACGC  
GAAGGGACGCAGTCAACGTCAGACGGAGAAGCAGACCAAAAAACAAAGGAGTGCGCA  
AAGGTACTGTGAGCTGGAGGAAAAGCACTGCTGCTGCATAAGAAAGTAACGGACCCA  
AATGTTCCAGAATATGCATATTCAAATTTTGGTGTAGTTTTCTGTACACTGTCCATT  
CATTATCTTATCAGTACAAGTGTAAACGAGACATGTCAGAAAGTCGAAGGTTGTGC  
GTAATTTGATAAGCATTGTTTACTGGGACGAACGGA (SEQ ID NO:242)

**Translation:**

MSGLGIMVLTLLLLVSMATSHRYAREKQATRRDAVNVRRRSRPKTKECERYCELEEKH  
CCCIRSNPKKSRICIFKFWC (SEQ ID NO:243)

**Toxin Sequence:**

Xaa3-Lys-Thr-Lys-Xaa1-Cys-Xaa1-Arg-Xaa5-Cys-Xaa1-Leu-Xaa1-Xaa1-Lys-His-Cys-Cys-  
Cys-Ile-Arg-Ser-Asn-Gly-Xaa3-Lys-Cys-Ser-Arg-Ile-Cys-Ile-Phe-Lys-Phe-Xaa4-Cys-<sup>^</sup> (SEQ  
ID NO:244)

5 **Name:** Bromosleeper-T2  
**Species:** tulipa  
**Cloned:** Yes

**DNA Sequence:**

10 CAGGATTGAACAAAATTCAGGATGTCAGGATTGGAATCATGGTGCTAACCCCTTCT  
CCTTCTTGTGCTAATGACAACCAGTCATCAGGATGCAGGAGAGAAGCAGGCGATGC  
AAAGGGACGCAAAAGAACTTCAGTCGGAGAAGATTAGTCATTCGGAGACCAAAAAAC  
AAGGGAGTGCGAAATGCAGTGTGAGCAGGAGGAGAAACACTGCTGCCGCGTAAGA  
GATGGTACGGGGCAATGTGCCCTAAAGTGCTTGGGAATTAACCTGGTAGTTTCTGTAC  
5 ACTGTCTCATTCATTATCTTATCAGTACACGTGTAACGAGACATGTCAGAAAAGTCGA  
AGGTAGTGCGTAATTTGATAAGCATTGTTTACTGGGACGAACGGA (SEQ ID NO:245)

**Translation:**

20 MSGLGIMVLTL LLLVLMTTSHQDAGEKQAMQRDAKNFSRRRLVIRRPKTRCEMQCEQ  
EEKHCCRVRDGTGQCAPKCLGINW (SEQ ID NO:246)

**Toxin Sequence:**

25 Xaa3-Lys-Thr-Arg-Xaa1-Cys-Xaa1-Met-Gln-Cys-Xaa1-Gln-Xaa1-Xaa1-Lys-His-Cys-Cys-Arg-  
Val-Arg-Asp-Gly-Thr-Gly-Gln-Cys-Ala-Xaa3-Lys-Cys-Leu-Gly-Ile-Asn-Xaa4-<sup>^</sup> (SEQ ID  
NO:247)

**Name:** T8.1  
**Species:** tulipa  
**Cloned:** Yes

**DNA Sequence:**

30 ATGATGTCGAAAAATGGGAGCTATGTTTGCTCTTTTGCTCTTTTACCCTGGCATCCA  
GCCAGCAGGAAGGAGATGTCCAGGCAAGGAAAAACACGCCTGAAGAGCGACTTCTA  
TCGTGCTCTGCCAAGGTTTGGCCCAATATGCACCTGTTTTAAAGCCAGAACTGTGC  
35 GGGTTCTTGTAATGCATGTCACTCCCGGTTGTACTGCAGTAACAAATGGCATTCTG  
TGAACGAGGATGCTCGTGTACATGTCCAGGGACTGGTTGAATGATTGAAAAATTC  
AGAGCAATATGTTGCAGAAAAACCGAAGACCGAGACTTCTACAATAAATCCATAA  
AGACATTA AAAAAAAAAAAAAAAAAA (SEQ ID NO:248)

**Translation:**

40 MMSKMGAMFVLLLLFTLASSQQEGDVQARKTRLKSDFYRALPRFGPICTCFKSQNCRG  
SCECMSPPGCYCSNNGIRERGCSTCPGTG (SEQ ID NO:249)

**Toxin Sequence:**

45 Phe-Gly-Xaa3-Ile-Cys-Thr-Cys-Phe-Lys-Ser-Gln-Asn-Cys-Arg-Gly-Ser-Cys-Xaa1-Cys-Met-  
Ser-Xaa3-Xaa3-Gly-Cys-Xaa5-Cys-Ser-Asn-Asn-Gly-Ile-Arg-Xaa1-Arg-Gly-Cys-Ser-Cys-Thr-  
Cys-Xaa3-Gly-Thr-# (SEQ ID NO:250)

10072602.021102

**Name:** T8.2  
**Species:** tulipa  
**Cloned:** Yes

**DNA Sequence:**

ATGATGTCGAAAAATGGGAGCTATGTTTGTCCTTTTGCTTCTTTTACCCCTGGCATCCA  
 GCCAGCAGGAAGGAGATGTCCAGGCAAGGAAAAACACGCCTGAAGAGCGACTTCTA  
 TCGTACTCTGGCAATATCTGACAGAGGATGCACTGGCAACTGTGATTGGACGTGTA  
 GCGGTGATTGCAGCTGCCAGGGCACATCTGACTCGTGTCCTGCAATCCACCAAAAAT  
 CAATAGGCAACAGATGCCGGTGTCAAGTGTAAAAAGAAAAATCGAAATTGACTGATTC  
 TTTTAACTCGTTGAACGATTAAAAAATCAGACCAATATGTAGGCAGAAAAACCGAAG  
 ACTCTGAGACTCTCGTAATAATCGTAAGCAAAAAAAAAAAAAAAAAA (SEQ ID NO:251)

**Translation:**

MMSKMGAMFVLLLLFTLASSQEQEGDVQARKTRLKSDFYRTLAISSDRGCTGNCDWTCS  
 GDSCSQGTSDSCHIPPKSIGNRCRCQCKRKIEID (SEQ ID NO:252)

**Toxin Sequence:**

Gly-Cys-Thr-Gly-Asn-Cys-Asp-Xaa4-Thr-Cys-Ser-Gly-Asp-Cys-Ser-Cys-Gln-Gly-Thr-Ser-  
 Asp-Ser-Cys-His-Cys-Ile-Xaa3-Xaa3-Lys-Ser-Ile-Gly-Asn-Arg-Cys-Arg-Cys-Gln-Cys-Lys-  
 Arg-Lys-Ile-Xaa1-Ile-Asp-^ (SEQ ID NO:253)

**Name:** Vr6.1  
**Species:** virgo  
**Cloned:** Yes

**DNA Sequence:**

GGATCCATGAAACTGACGTGTGTGGTGATCATCACTGTGCTGTTCTCTGACGGCCAGT  
 CAGCTCATTACAGCTGATTACTCCAGAGATCAGCGGCAGTACCGTGCACTGAGGTT  
 GGGAGATGAAATGCGGAATTTCAAAGGTGCCAGGACTGCGGGGGACAAGGTGAA  
 GGTGTATATACTCAACCTTGCTGCCCTGGTCTGCGGTGCCGTGGCGGCGGTACTGGA  
 GGAGGCGTATGCCAGCTGTAGTAATAGTTTGGCATCTGATATTTCCCTCTGTGCTC  
 CACCCTCTTTGCCTGATTATCCTTACCTATGTGTGGTCATGAACCACTCAGTAGCT  
 ACACCTCTGGTGGATTACAGAGAACGTATATCAAAATAAAACCACATTGCAATAAAAA  
 AAAAAAAAA (SEQ ID NO:254)

**Translation:**

MKLTCVVITVFLFTASQLITADYSRDQRQYRAVRLGDEMRFKRGARDCGGQGEHCYT  
 QPCCPGLRCRGGGTGGGVCQL (SEQ ID NO:255)

**Toxin Sequence:**

Asp-Cys-Gly-Gly-Gln-Gly-Xaa1-Gly-Cys-Xaa5-Thr-Gln-Xaa3-Cys-Cys-Xaa3-Gly-Leu-Arg-  
 Cys-Arg-Gly-Gly-Gly-Thr-Gly-Gly-Gly-Val-Cys-Gln-Leu-^ (SEQ ID NO:256)

**Name:** R6.9  
**Species:** radiatus

**Cloned:** Yes

**DNA Sequence:**

ATCATGCAGAAACTGACAATCCTGCTTCTTGTTGCTGCTATACTGATGTCGACCCAG  
 GTCCTGATTCAAGGTGGTGGAGAAAAACGCCAAAAAGTCAACATTTTTCAAAAAG  
 AAAGACAGATGCTGAGACCTGGTGGGAGGGCGAATGCTCTAATTGGTTAGGAAGTT  
 GTTCGACGCCCTCAAATTGCTGTCTCAAGAGTTGTAATGGGCACTGCACATTGTGGT  
 GATGAACTCTGACCACAAAGCCATCCAACATCACCGCTCTCCTCTTCAGAGTCTTCA  
 AG (SEQ ID NO:257)

**Translation:**

MQKLTIILLVAAILMSTQVLIQGGGEKRQKVNIKSKRKTD AETWWEGECSNLGSCST  
 PNNCLKSCNGHCTLW (SEQ ID NO:258)

**Toxin Sequence:**

Xaa4-Xaa4-Xaa1-Gly-Xaa1-Cys-Ser-Asn-Xaa4-Leu-Gly-Ser-Cys-Ser-Thr-Xaa3-Ser-Asn-Cys-  
 Cys-Leu-Lys-Ser-Cys-Asn-Gly-His-Cys-Thr-Leu-Xaa4-<sup>^</sup> (SEQ ID NO:259)

**Name:** R6.10  
**Species:** radius  
**Cloned:** Yes

**DNA Sequence:**

ATCATGCAGAAACTGATAATCCTGCTTCTTGTTGCTGCTGTACTGATGTCCACCCAG  
 GCCCTGATTCAAGGTGGTGGAGAAAAACGCCAACAGGCAAAAGCAAGTATTTTC  
 CGAAAGAAAGGCACCTGCTAAGCGTTGGTTTGGACACGAAGAATGCACTTATTGGT  
 TGGGGCCTTGTGAGGTGGACGACACGTGTTGTTCTGCCAGTTGTGAGTCCAAGTTCT  
 GCGGGTTGTGGTGATGGACACTGACCACAAGTCATCTACATCGCCACTCTCCTGTT  
 CAGAGTCTTCAAG (SEQ ID NO:260)

**Translation:**

MQKLIIILLVAAVLMSTQALIQQGGGKRQQA KSKYFSEKAPAKRWFGEECTYWLGP  
 CEVDDTCCSASCESKFCLW (SEQ ID NO:261)

**Toxin Sequence:**

Xaa4-Phe-Gly-His-Xaa1-Xaa1-Cys-Thr-Xaa5-Xaa4-Leu-Gly-Xaa3-Cys-Xaa1-Val-Asp-Asp-  
 Thr-Cys-Cys-Ser-Ala-Ser-Cys-Xaa1-Ser-Lys-Phe-Cys-Gly-Leu-Xaa4-<sup>^</sup> (SEQ ID NO:262)

**Name:** W16.1  
**Species:** wittigi  
**Cloned:** Yes

**DNA Sequence:**

GGATCCATGAAACTGACGTGTGTGGTGATCATCGCCTTGCTGTTCTCTGACGGCCTGT  
 CAGCTCATTACGGCTGATTACTCCAGAGATGAGCAGTCTGGCAGTACAGTGC GGTTT  
 CTAGACAGACCACGGCGTTTGGTTTCGTTCAACCGTGCGCCCGTTTAGGTGAACCA

1072603.02112

TGTACCATATGCTGCCGTCCTTTGAGGTGCCGTGAAAGCGGAACACCCACATGTCAA  
GTGTGATTGTCTGGCATCTGATATTTCCCCTCTGTGGCCTACCCTCTTTGCCTGAGT  
CATCCATACCTGTGCTCGAG (SEQ ID NO:263)

**Translation:**

MKLTCVVIIALLFLTACQLITADYSRDEQSGSTVRFLDRPRRFGSFIPCARLGEPCTICCRP  
LRCRESGTPTCQV (SEQ ID NO:264)

**Toxin Sequence:**

Phe-Gly-Ser-Phe-Ile-Xaa3-Cys-Ala-Arg-Leu-Gly-Xaa1-Xaa3-Cys-Thr-Ile-Cys-Cys-Arg-Xaa3-  
Leu-Arg-Cys-Arg-Xaa1-Ser-Gly-Thr-Xaa3-Thr-Cys-Gln-Val-^ (SEQ ID NO:265)

**Name:** Rg6.6  
**Species:** regius  
**Cloned:** Yes

**DNA Sequence:**

GGATCCATGAAACTGACGTGCGTGGTGATCATGGCCTCGCTGTTCTGGCGGCCTGT  
CAATTCCTTACAGCTGGAGGTGACTCAAGAAGTAAGCAGCGGTATCCTGATTGGAG  
GCTGGGCTACCGAAAGTCCAAGTTGATGGCTAAGAAGACGTGCCTGGAACATAACA  
AACTATGTTGGTATGATAGAGACTGCTGCACCATATATTGTAATGAAAACAAATGC  
GGCGTGAAACCTCAATGAATGTTTCACACACACACACACACACACACACACACA  
CACACACACACACACACACACACACACATCTGGCGTCTGACCATTCCCCCTCTGT  
GCTCTATCCTCTGTTCTCTGAGTCATCCATACCTGTGCTCGAG (SEQ ID NO:266)

**Translation:**

MKLTCVIMASFLAACQFLTAGGDSRSKQRYPDWRLGYRKSCLMAKKTCLHNKLC  
WYDRDCCTIYCENENKCGVKPQ (SEQ ID NO:267)

**Toxin Sequence:**

Thr-Cys-Leu-Xaa1-His-Asn-Lys-Leu-Cys-Xaa4-Xaa5-Asp-Arg-Asp-Cys-Cys-Thr-Ile-Xaa5-  
Cys-Asn-Xaa1-Asn-Lys-Cys-Gly-Val-Lys-Xaa3-Gln-^ (SEQ ID NO:268)

**Name:** R6.9  
**Species:** radiatus  
**Cloned:** Yes

**DNA Sequence:**

ATCATGCAGAAACTGACAATCTGCTTCTTGTGCTGCTATACTGATGTCGACCCAG  
GTCCTGATTCAAGGTGGTGGAGAAAAACGCCAAAAAGTCAACATTITTTCAAAAAG  
AAAGACAGATGCTGAGACCTGGTGGGAGGGCGAATGCTCTAATTGGTTAGGAAGIT  
GTTTCGACGCCCTCAAATTGCTGTCTCAAGAGTTGTAATGGGCACTGCACATTGTGGT  
GATGAACCTGTGACCACAAAGCCATCCAACATCACCGCTCTCTCTTCAGAGTCTTCA  
AG (SEQ ID NO:269)

**Translation:**

MQKLTILLLVAAILMSTQVLIQGGGEKRQKVNIFSKRKTD AETWWEGECSNWLGCST  
PSNCLKSCNGHCTLW (SEQ ID NO:270)

5 **Toxin Sequence:**

Xaa4-Xaa4-Xaa1-Gly-Xaa1-Cys-Ser-Asn-Xaa4-Leu-Gly-Ser-Cys-Ser-Thr-Xaa3-Ser-Asn-Cys-  
Cys-Leu-Lys-Ser-Cys-Asn-Gly-His-Cys-Thr-Leu-Xaa4-<sup>^</sup> (SEQ ID NO:271)

10 **Name:** R6.10  
**Species:** radiatus  
**Isolated:** Yes  
**Cloned:** Yes

5 **DNA Sequence:**

ATCATGCAGAAACTGATAATCCTGCTTCTTGTTGCTGCTGCTACTGATGTCCACCCAG  
GCCCTGATTCAAGGTGGTGGAGGAAAACGCCAACAGGCAAAGAGCAAGTATTTTTC  
CGAAAGAAAAGGCACCTGCTAAGCGTTGTTTGGACACGAAGAATGCACCTATGTT  
TGGGGCCTTGTGAGGTGGACGACACGTGTTGTTCTGCCAGTTGTGAGTCCAAGTTCT  
GCGGGTTGTGGTGATGGACACTGACCACAAGTCATCCTACATCGCCACTCTCCTGTT  
CAGAGTCTTCAAG (SEQ ID NO:272)

**Translation:**

MQKLIILLLVAAVLMSTQALIQGGGKRRQAKSKYFSEKAPAKRWFGHBECTYWLGP  
CEVDDTCCSASCESKFCGLW (SEQ ID NO:273)

**Toxin Sequence:**

Xaa4-Phe-Gly-His-Xaa1-Xaa1-Cys-Thr-Xaa5-Xaa4-Leu-Gly-Xaa3-Cys-Xaa1-Val-Asp-Asp-  
Thr-Cys-Cys-Ser-Ala-Ser-Cys-Xaa1-Ser-Lys-Phe-Cys-Gly-Leu-Xaa4-<sup>^</sup> (SEQ ID NO:274)

30 **Name:** Sf.5.1  
**Species:** spurius  
**Cloned:** Yes

35 **DNA Sequence:**

GGAAGCTGACTACAAAGCAGAATGCGCTGTCTCCAGTCTTCGTGCTATTCTTCTGCTGC  
TGATTCATCTGCACCTAGCACTGATGCCGACCCGAAGACCAAAGATGATGTGCGC  
CTGGCATCTTTCCACGGTAAGGCAAAGCGAACCTACAAATACCTAGGGGGAATAT  
CCAATGTTGCACAAAATATCAGCCGTGCTGTTCTTACCATCATAAAGGGAAATGAC  
TTTGATGAGACCCCTGCGAACTGTCCTTGGATGTGAAATTTGAAAACGAGACTGTTT  
CTTTCGCGCGTGTTCGTGGAATTTCGAATGGTCGTTAATAACACGCTGCCTCTTGCA  
AACTACAATCTCTCTGTCCTTTATCTGTGGACTGGATGTCAACACTG (SEQ ID  
NO:275)

45 **Translation:**

MRCLPVFVILLLLIPSAPSTDARPKTKDDVRLASFHGKAKRTLQIPRGNIHCCTKYQPCC  
SSPS (SEQ ID NO:276)

**Toxin Sequence:**

5 Gly-Asn-Ile-His-Cys-Cys-Thr-Lys-Xaa5-Gln-Xaa3-Cys-Cys-Ser-Ser-Xaa3-Ser-<sup>^</sup> (SEQ ID NO:277)

**Name:** Nb5.1

10 **Species:** nobilis

**Cloned:** Yes

**DNA Sequence:**

ATGCGCTGTCTCCCAGTCTTCGTCATTCTTCTGCTGCTGACTGCATCTGCACCAAGCG  
TTGATGCCCGACCGAAGACCAAAGATGATGTGCTCCGGGCATCTTCCGCGATAAT  
GCAAAGAGTACCTTACAAAGACTTTGGAACAAACGCATCTGCTGCCCCATAATTCTT  
TGGTGTGTGGTTAACCAGCATGAAGTTCCAGGA (SEQ ID NO:278)

**Translation:**

MRCLPVFVILLLLTASAPSVDARPKTKDDVLRASFRDnakSTLQRLWNKRICCPILWCC  
G (SEQ ID NO:279)

**Toxin Sequence:**

Ile-Cys-Cys-Xaa3-Ile-Ile-Leu-Xaa4-Cys-Cys-# (SEQ ID NO:280)

**Name:** Bt5.1

**Species:** betulinus

**Cloned:** Yes

**DNA Sequence:**

ATGCGCTGTCTCCCAGTCTTCATCATTCTTCTGGTGCTGATTGCATCTGCACCTACCG  
TTGATGCCCGACCAAAGATCGAAGATGATGAGTCCCTGGCATCTTCCATGNTCATN  
AACCACCATNANNNGTNCANCTTTTGAACAAACGCAATTGCTGCCCAGACTCTCCTC  
CGTGCTGTCTAACCAGCATGAAGTTCAGGA (SEQ ID NO:281)

**Translation:**

MRCLPVFILLVLIASAPTVDARPKIEDDESASFH?H?PP????LLNKRNCPPDSPPCCH  
(SEQ ID NO:282)

**Toxin Sequence:**

Asn-Cys-Cys-Xaa3-Asp-Ser-Xaa3-Xaa3-Cys-Cys-His-<sup>^</sup> (SEQ ID NO:283)

**Name:** t-PVA

**Species:** purpurascens

**Isolated:** Yes

**Cloned:** Yes

**DNA Sequence:**

GGAATTCCAAATGATGTAATTACTGACTACATGGTCATAGTGTATACCCATTGAAAA  
 ATTTCTATGACATTTTCAGTTGTTAGATCATCCAGTTCCACAGATGGAAAGACAGAGA  
 GATAGTAGCTTGCAAGTGGCAGCGTGTGTTAACGACCATTGACATTCCATGAACA  
 CGTGTGAAAGGAGCAGTCTGCTTTCCAAATCTGACATCCAGGGACAGTTTGCAGGG  
 GTCTCATCCAAAGTCATCTTCTTTATCCCAAAGTACAGCACCGCATCTGTTTGGGA  
 CAGCAACCGCGTTTCTTCCAAAATCTTTGTAGGGTTCTTTTGCATTATCGTGGAAA  
 GATGCCAGGGGCATATCATCTTTGGTCTTCGGATGAGCATCAACGCAAGGTGCAGA  
 TGGAATCAGCAGCAGAAGAATGACGAAGACTGGCAGACAGCGCATTCTGCTTGTAG  
 TCAGCTTCCGAATTCCAAGCCGAATTCTGCAGATATCCATCACACTGGCGGCCGCTC  
 GAGCATGCATCTAGAGGGCCCAATTCGCCCTATAGTGAGTCGTATGACAATTCAcTG  
 GC (SEQ ID NO:284)

**Translation:**

MRCLP VFVILLLLIPSA PCVDAHPKTKDDMPLASFHDNAKGLRQFWKKRGCCPKQMR  
 CCTLG (SEQ ID NO:285)

**Toxin Sequence:**

Gly-Cys-Cys-Xaa3-Lys-Gln-Met-Arg-Cys-Cys-Thr-Leu-# (SEQ ID NO:286)

**Name:** Af5.2

**Species:** ammiralis

**Cloned:** Yes

**DNA Sequence:**

GGAAGCTGACTACAAGCAGAATGCACTGTCTCCAGTCGTCGTCTATTCTTCTGCTGC  
 TGA CTGCATCTGGTGGACCTAGCGTTGATGCCCGACTGAAAGACCAAAGATGATGTG  
 CCCCTGTCATCTTCCGCGATAATACAAAGAGTATCTACAAAGACTTTGGAAGCGA  
 GGCAACTGCTGTGAATTTGGGAGTITTGCTGTGATTAACCAAGCATGAAGG (SEQ ID  
 NO:287)

**Translation:**

MHCLPVVVILLLLTASGGPSVDARLKTDDVPLSSFRDNTKSIQLRWKRGNCCEFWF  
 CCD (SEQ ID NO:288)

**Toxin Sequence:**

Gly-Asn-Cys-Cys-Xaa1-Phe-Xaa4-Xaa1-Phe-Cys-Cys-Asp-^ (SEQ ID NO:289)

**Name:** Da5.1

**Species:** dalli

**Cloned:** Yes

**DNA Sequence:**

GGAAGCTGACTACAAGCAGAATGCACTGTCTCCAGTCTTCGTCATTCTTCTGCTGC  
TGACTGCATCTGGACCTAGCGTTGATGCCCAACCGAAGACCGAAGTTGATGTGCC  
CTGTGCATCTTTCCGCGATAATGCAAAGCGTGCCCTACAAAGACTTCCGCGTTGCTGT  
GAATATTGGAAGTTGTGCTGTGGTTAACCAGCATGAAGG (SEQ ID NO:290)

**Translation:**

MHCLP VFVILLLLTASGPSVDAQPKTEVDVPLSSFRD NAKRALQRLPRCCEYWKLCGG  
(SEQ ID NO:291)

**Toxin Sequence:**

Cys-Cys-Xaa1-Xaa5-Xaa4-Lys-Leu-Cys-Cys-# (SEQ ID NO:292)

**Name:** Om5.1  
**Species:** omaria  
**Cloned:** Yes

**DNA Sequence:**

GGAAGCTGACTACAAGCAGAATGCGCTGTCTCCAGTCTTCGTCATTCTTCTGCTGC  
TAACTGCATCTGCACCTAGCGTTGATGCCCACCGAAGGCCAAAGATGATGTGCC  
CTGGCATCTTTCCGCGATAATGCAAAGAGTACCCTACAAAGACTTCAGGACAAACG  
CGTTTGTCTGGCTATAAGTTTTTTGTCTGTCGTTAACCAGCATGAAGG (SEQ ID  
NO:293)

**Translation:**

MRCLP VFVILLLLTASAPSV DARPKAKDDVPLASFRD NAKSTLQRLQDKRVCCGYKFFC  
CR (SEQ ID NO:294)

**Toxin Sequence:**

Val-Cys-Cys-Gly-Xaa5-Lys-Phe-Phe-Cys-Cys-Arg-^ (SEQ ID NO:295)

**Name:** Au5.1  
**Species:** aulicus  
**Cloned:** Yes

**DNA Sequence:**

GGAAGCTGACTACAAGCAGAATGCGCTGTCTCCAGTCTTCGTCATTCTTCTGCTGC  
TGACTGCATCTGCACCTAACGTTGATGCCCAACCGAAGACCAAAGATGATGTGCC  
CTGGCATCTTTGCACGATGATGCAAAGAGTGCACTACAACATTGGAACCAACGCTG  
CTGCCCCATGATCTATTGGTGCTGTAGTTAACCAGCATGAAGG (SEQ ID NO:296)

**Translation:**

MRCLP VFVILLLLTASAPNVDAQPKTKDDVPLASLHDDAKSALQHWNRCCPMIYWC  
CS (SEQ ID NO:297)

**Toxin Sequence:**

Cys-Cys-Xaa3-Met-Ile-Xaa5-Xaa4-Cys-Cys-Ser-^ (SEQ ID NO:298)

**Name:** Au5.4  
**Species:** aulicus  
**Cloned:** Yes

**DNA Sequence:**

GGAAGCTGACTACAAGCAGAATGCACTGTCTCCAGTCTTCGTCATTCTTCTGCTGC  
 TGACTGCATCTGCACCTAACGTTGATGCCCAACCGAAGACCAAAGATGATGTGCC  
 CTGGCATCTTTGCACGATGATGCAAAGAGTGCACTACAACATTGGAACCAACGCTG  
 CTGCCCCGAGATCTATTGGTGCTGTAGTTAACCAGCATGAAGG (SEQ ID NO:299)

**Translation:**

MHCLPVPFVILLLLTASAPNVDAQPKTKDDVPLASLHDDAKSALQHWNRCCPEIYWCC  
 S (SEQ ID NO:300)

**Toxin Sequence:**

Cys-Cys-Xaa3-Xaa1-Ile-Xaa5-Xaa4-Cys-Cys-Ser-^ (SEQ ID NO:301)

**Name:** Af5.1  
**Species:** ammiralis  
**Cloned:** Yes

**DNA Sequence:**

GGAAGCTGACTACAAGCAGAATGCGCTGTCTCCAGTCTTCGTCATTCTTCTGCTGC  
 TGATTGCATCTGCACCTAGCGTTGATGCCCAACCGAAGACCAAAGATGATGTGCC  
 TGGCATCTTTGCACGATAATATAAAGAGTACTCTACAAACACTTTGGAACAAACGCT  
 GCTGCCCCCTGTGATTGGTGCTGTGGTTAACCAGCATAAAGG (SEQ ID NO:302)

**Translation:**

MRCLPVPFVILLLLIASAPSVDAQPKTKDDVSLASLHDNIKSTLQTLWNRCCPPVIWCCG  
 (SEQ ID NO:303)

**Toxin Sequence:**

Cys-Cys-Xaa3-Xaa3-Val-Ile-Xaa4-Cys-Cys-# (SEQ ID NO:304)

**Name:** Au5.3  
**Species:** aulicus  
**Cloned:** Yes

**DNA Sequence:**

GGAAGCTGACTACAAGCAGAATGCGCTGTCTCCAGTCTTCGTCATTCTTCTGCTGC  
 TGACTGCATCTGGACCTAGCGTTGATGCCCGACCGAAGACCAAAGATGATGTGCCT

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CTGTCACTCTTTCCGCGATAACGCAAAGAGTATCCTACAAAGACGTTGGAACAACATAT  
TGCTGCACGAATGAGCTTGGTGCTGTGGTTAACCAGCATGAAGG (SEQ ID NO:305)

**Translation:**

MRCLPVPFVILLLLTASGPSVDARPKTKDDVPLSSFRDNAKSILQRRWNNYCCTNELWCC  
G (SEQ ID NO:306)

**Toxin Sequence:**

Xaa4-Asn-Asn-Xaa5-Cys-Cys-Thr-Asn-Xaa1-Leu-Xaa4-Cys-Cys-# (SEQ ID NO:307)

**Name:** Da5.2

**Species:** dalli

**Cloned:** Yes

**DNA Sequence:**

GGAAGCTGACTACAAGCAGAATGCACTGTCTCCAGTCTTCGTCATTCTTCTGTCTGC  
TGACTGCATCTGGACCTAGCGTTGATGCCCGACCGAAGACCGAAGATGATGTGCC  
CTGTCATCTTTCCGCGATAATACAAAGAGTACCCTACAAAGACTTTTGAAGCCAGTC  
AACTGCTGTCCTATTGATCAATCTTGCTGTTCTTAACCAGCATGAAGG (SEQ ID  
NO:308)

**Translation:**

MHCLPVPFVILLLLTASGPSVDARPKTEDDVPLSSFRDNTKSTLQRLKPVNCCPIDQSCC  
S (SEQ ID NO:309)

**Toxin Sequence:**

Xaa3-Val-Asn-Cys-Cys-Xaa3-Ile-Asp-Gln-Ser-Cys-Cys-Ser-^ (SEQ ID NO:310)

**Name:** Cn10.3

**Species:** consors

**Cloned:** Yes

**DNA Sequence:**

GGATCCATGTTACCGTGTTTCTGTTGGTGTCTTGGAACCACTGTCGTTTCCATCC  
CTTCAGATCGTGATCTGAAGGCAGGAATGCCGTAGTCCACGAGAGAGCGCCTGAG  
CTGGTCGTTACGGCCACCACGACTTGCTGTGGTTATGATCCGATGACAATATGCCCT  
CCTTGCATGTGCACTCATTCTGTCCACCAAAAAGAAAACCAGGCCGAGAAACGA  
CTGATGCTCGAG (SEQ ID NO:311)

**Translation:**

MFTVFLLVVLATTVVSIPSDRASEGRNAVVHERAPELVVITATTCCGYDPMITCPCMC  
THSCPPKRKPGRND (SEQ ID NO:312)

**Toxin Sequence:**

Ala-Xaa3-Xaa1-Leu-Val-Val-Thr-Ala-Thr-Thr-Thr-Cys-Cys-Gly-Xaa5-Asp-Xaa3-Met-Thr-Ile-  
Cys-Xaa3-Xaa3-Cys-Met-Cys-Thr-His-Ser-Cys-Xaa3-Xaa3-Lys-Arg-Lys-Xaa3-# (SEQ ID  
NO:313)

5

**Name:** A10.2  
**Species:** aurisiacus  
**Cloned:** Yes

10 **DNA Sequence:**

GGATCCATGTTACACCGTGTCTGTTGGTTGTCTTGGCAACCACTGTCGTTTCCATCC  
CTTCAGATCGTGCATCTGATGGCAGGAATGCCGAGTCAACGAGAGACAATCTTGG  
CTGGTCCCTTCGACAATCAGCACTTGCTGTGGATATGATCCGGGGACAATGTGCCCT  
CCTTGCAGGTGCAATAATACCTGTAAACCAAAAAAAAAACCAAAACCAGGAAAAGGCC  
GCAGAAACGACTGATGCTCCAGGACCCTCTGAACCACGACCTCGAG (SEQ ID  
NO:314)

**Translation:**  
MFTVFLLVVLATTVVSIPSDRASDGRNAAVNERQSWLVPSTITTCGGYDPGTMCPPCRC  
NNTCKPKPKPKGRRND (SEQ ID NO:315)

25 **Toxin Sequence:**

Xaa2-Ser-Xaa4-Leu-Val-Xaa3-Ser-Thr-Ile-Thr-Thr-Cys-Cys-Gly-Xaa5-Asp-Xaa3-Gly-Thr-  
Met-Cys-Xaa3-Xaa3-Cys-Arg-Cys-Asn-Asn-Thr-Cys-Lys-Xaa3-Lys-Lys-Xaa3-Lys-Xaa3-Gly-  
Lys-# (SEQ ID NO:316)

**Name:** Cn10.4  
**Species:** consors  
**Cloned:** Yes

30 **DNA Sequence:**

GGATCCATGTTACACCGTGTCTGTTGGTTGTCTTGGCAACCACTGTCGTTTCCATCC  
CTTCAGATCGTGCATCTGATGGCAGGAATGCCGAGTCCACGAGAGAGCGCCTGAG  
CTGGTCGTACCGCCACCACGACTTGCTGTGGTTATGATCCGATGACATGGTGCCTT  
TCTTGCATGTGCACTTATTCCTGTCCCCACCAAGGAAAAAACAGGCCGAGAAA  
CGACTGATGCTCCAGGACCCTCTGAACCACGACCTCGAG (SEQ ID NO:317)

**Translation:**  
MFTVFLLVVLATTVVSIPSDRASDGRNAVVERAPELVVTATTTCCGYDPMTWCPSCM  
CTYSCPHQRKKPGRRND (SEQ ID NO:318)

40 **Toxin Sequence:**

Ala-Xaa3-Xaa1-Leu-Val-Val-Thr-Ala-Thr-Thr-Thr-Cys-Cys-Gly-Xaa5-Asp-Xaa3-Met-Thr-  
Xaa4-Cys-Xaa3-Ser-Cys-Met-Cys-Thr-Xaa5-Ser-Cys-Xaa3-His-Gln-Arg-Lys-Lys-Xaa3-# (SEQ  
ID NO:319)

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**Name:** M10.3  
**Species:** magus  
**Cloned:** Yes

**DNA Sequence:**

GGATCCATGTTACCGTGTTTCTGTTGGTTGTCTGGCAACCAAGTGTCTGTTCCATCC  
 CTTGATCGTGCATCTGATGGCGGAATGCCGTAGTCCACGAGAGAGCGCCTGAG  
 CTGGTCGTTACGCCACCAACGACTTGCTGTGGTTATGATCCGATGACAATATGCCCT  
 CCCTGCATGTGCACTCATTCCTGTCCACCAAAGGAAAACAGGCCGCAGGAACGA  
 CTGATGTCCAGGACCTCTGAACCACGACNCGAG (SEQ ID NO:320)

**Translation:**

MFTVFLLVLATSVVSIPSDRASDGGNAVVHERAPELVVTATTTCGYDPMTCPPCMC  
 THSCPPKKGKPGRRND (SEQ ID NO:321)

**Toxin Sequence:**

Ala-Xaa3-Xaa1-Leu-Val-Val-Thr-Ala-Thr-Thr-Thr-Cys-Cys-Gly-Xaa5-Asp-Xaa3-Met-Thr-Ile-  
 Cys-Xaa3-Xaa3-Cys-Met-Cys-Thr-His-Ser-Cys-Xaa3-Xaa3-Lys-Gly-Lys-Xaa3-# (SEQ ID  
 NO:322)

**Name:** A10.3  
**Species:** aurisiacus  
**Cloned:** Yes

**DNA Sequence:**

GAATTCGCCCTTGAGGATCCGTGTGGTCTGGGTCCAGAACCTGATGGCAGGAATG  
 CCGCAGTCAACGAGAGACAGAAATGGCTGGTCCATTGCAAAATCACGTATTGCTGT  
 GGTATAATAAGATGGACATGTGCCCTCCTTGATGTGCACTTATCCTGTCCCCC  
 CTAAGAAAAAAGACAGGCCGCAGAAACGACTGATGCTCCAGGACCTCTGAA  
 CCACGACCTCGAGCGAAGGGCGGAATTC (SEQ ID NO:323)

**Translation:**

VVLGPEPDGRNAAVNERQKWLVHSKITYCCGYNKMDMCPPCMCTYSCPLKKKRPGR  
 RND (SEQ ID NO:324)

**Toxin Sequence:**

Xaa2-Lys-Xaa4-Leu-Val-His-Ser-Lys-Ile-Thr-Xaa5-Cys-Cys-Gly-Xaa5-Asn-Lys-Met-Asp-Met-  
 Cys-Xaa3-Xaa3-Cys-Met-Cys-Thr-Xaa5-Ser-Cys-Xaa3-Xaa3-Leu-Lys-Lys-Lys-Arg-Xaa3-#  
 (SEQ ID NO:325)

**Name:** A10.4  
**Species:** aurisiacus  
**Cloned:** Yes

**DNA Sequence:**

GAATTCGCCCTTGAGGATCCGTGTGTTCTGGGTCCAGCATTGATGGCAGGAATGC  
 CGCAGTCAACGAGAGAGCGCCTTGACGGTCTGTACGGCCACCACGAATTGCTGCG  
 GTATTACCGGGCCAGGCTGCCTTCCTTGCCGTTGTAACAACATGTGGCTGATGCT  
 CCAGGACCCTCTGAACCACGACCTCGAGCGAAGGGCGAATTC (SEQ ID NO:326)

**Translation:**

VVLGPAFDGRNAAVNERAPWTVVTATTNCCGITGPGCLPCRCTQTCG (SEQ ID  
 NO:327)

**Toxin Sequence:**

Ala-Xaa3-Xaa4-Thr-Val-Val-Thr-Ala-Thr-Thr-Asn-Cys-Cys-Gly-Ile-Thr-Gly-Xaa3-Gly-Cys-  
 Leu-Xaa3-Cys-Arg-Cys-Thr-Gln-Thr-Cys-# (SEQ ID NO:328)

Name: Mr1.3  
 Species: marmoreus  
 Cloned: Yes

**DNA Sequence:**

GGAAGCTGACTACAAGCAGAATGCGCTGTCTCCAGTCTTGATCATTCTTCTGCTGC  
 TGACTGCATCTGCACCTGGCGTTGTTGTCTACCGAAGACCGAAGATGATGTGCCCCA  
 TGTCATCTGTCTACGGTAATGGAAAGAGTATCCTACGAGGGATTCTGAGGAACGGT  
 GTTTGCTGTGGCTATAAGTTGTGCCTTCCATGTTAACCAGCATGAAGG (SEQ ID  
 NO:329)

**Translation:**

MRCLPVLIIILLLTASAPGVVLPKTEDDVPMSVVYNGKSILRGILRNGVCCGYKLCLP  
 C (SEQ ID NO:330)

**Toxin Sequence:**

Asn-Gly-Val-Cys-Cys-Gly-Xaa5-Lys-Leu-Cys-Leu-Xaa3-Cys-^ (SEQ ID NO:331)

Name: Pn1.5  
 Species: pennaceus  
 Cloned: Yes

**DNA Sequence:**

GGAATTCGGAAGCTGACTACAAGCAGAATGCGCTGTCTCCAGTCTTCGTCATTCTT  
 CTGCTGCTGACTGCATCTGCACCTAGCGTTGATGCCAAAGTTTCATCTGAAGACCAAA  
 GGTGATGGGCCCCTGTCACTTTCCGAGATAATGCAAAGAGTACCCTACAAAGACTT  
 CAGGACAAAAGCACTTGCTGTGGCTTTAAGATGTGTATCCCTTGTAGTTAACCAGCA  
 TGAAGGATCC (SEQ ID NO:332)

**Translation:**

MRCLPVFVILLLLTASAPSVDAKVHLKTKGDGPLSSFRDPAKSTLQRLQDKSTCCGFKM  
CIPCS (SEQ ID NO:333)

**Toxin Sequence:**

Ser-Thr-Cys-Cys-Gly-Phe-Lys-Met-Cys-Ile-Xaa3-Cys-Ser-<sup>^</sup> (SEQ ID NO:334)

**Name:** Pn1.6  
**Species:** pennaceus  
**Cloned:** Yes

**DNA Sequence:**

GAATTCGGAAGCTGACTACAAGCAGAATGCGTTGTCTCCCAGTCTTCGTCATTCTTC  
TGCTGCTGACTGCATCTGGACCTAGCGTTGATGCCCGACTGAAGACCAAAGATGAT  
GTGCCCTGTCTATCTTTCCGAGATAATGCAAAGAGTACCCTACAAAGACTTCAGGAC  
AAACGCCTTTGCTGTGGCTTTTGGATGTGTATTCCTTGAATTAACCAGCATGAAGG  
ATCC (SEQ ID NO:335)

**Translation:**

MRCLPVFVILLLLTASGPSVDARLTKDDVPLSSFRDPAKSTLQRLQDKRLCCGFWMCI  
PCN (SEQ ID NO:336)

**Toxin Sequence:**

Leu-Cys-Cys-Gly-Phe-Xaa4-Met-Cys-Ile-Xaa3-Cys-Asn-<sup>^</sup> (SEQ ID NO:337)

**Name:** Pn1.7  
**Species:** pennaceus  
**Cloned:** Yes

**DNA Sequence:**

GAATTCTCCCTTGGAAATTCTGAAGCTGACTACAANCAAGAATGCGTTGTCTCCCACTC  
TTCGTCTATTCTTCTGCTGCTGACTGCATCTGGACCTACTGTTGATGCCCAGCTGAAG  
ACCAAAGATGATGTGCCCTGTCTATCTTTCCGAGATAATGCAAAGAGTACCCTACA  
AAGACTTCAGGACAAAAGCACTTGTGTGGCTTTAAGATGTGTATTCCTTGTGGTTA  
ACCAGCATGAAGGATCC (SEQ ID NO:338)

**Translation:**

MRCLPLFVILLLLTASGPTVDARLTKDDVPLSSFRDPAKSTLQRLQDKSTCCGFKMCIP  
CG (SEQ ID NO:339)

**Toxin Sequence:**

Ser-Thr-Cys-Cys-Gly-Phe-Lys-Met-Cys-Ile-Xaa3-Cys-# (SEQ ID NO:340)

**Name:** Ep1.5  
**Species:** episcopatius

Cloned: Yes

**DNA Sequence:**

5 GAATTCGCCCTTGGGAATTCGGAAGCTGACTACAAGCAGAATGCGCTGTCTCCCAGTC  
TTCGTCATTCTCTGCTGCTGACTGCATCTGGACCTANTGTTGATGCCAAAGTTCATC  
TGAAGACCAAAGGTGATGGGCCCCCTGTCATCTTCCGAGATAATGCAAAGAGTACC  
CTACAAAGACTTCAGGACAAAAAGCACTTGCTGTGGCTATAGGATGTGTGTTCTTGT  
GGTTAACCAGCATGAAGGATCCV (SEQ ID NO:341)

10 **Translation:**

MRCLP VFVILLLLTASGPSVDAKVHLKTKGDPLSSFRD NAKSTLQRLQDKSTCCGYR  
MCVPCG (SEQ ID NO:342)

**Toxin Sequence:**

15 Ser-Thr-Cys-Cys-Gly-Xaa5-Arg-Met-Cys-Val-Xaa3-Cys-# (SEQ ID NO:343)

Name: Mr1.1

Species: marmoreus

20 Isolated: Yes

Cloned: Yes

**DNA Sequence:**

25 GGCGAATACACCTGGCAGGTA CTCAACGAACTTCAGGACACATTCTTTTACCTGGA  
CACTGGAACTGACAAACAGGCAGAATGCGCTGTCTCCCAGTCTTGATCATTCTTCTG  
CTGCTGACTGCATCTGCACCTGGCGTTGTTGTCCTACCGAAGACCGAAGATGATGTG  
CCCATGTCTCTGTCTACGTAATGGAAAGAGATCCTACGAGGAATTCTGAGGAA  
CGGTGTTTGCTGTGGCTATAAGTTGTGCCATCCATGTTAACCGACATGAAGGGAAAT  
GACTTTGGATGAGACCCCTGCGAACTGTCCCTGGATGTGAAATTTGGAAAGCAGAC  
30 TGTTCCTTTGCGACGTATTCGTGGAATTCGAATGGTCGTAACAACACGCTGCCAC  
TTGCAGGCTACTATCTCTGTCTTTCATCTGTGGAAATGGATGATCTAACAACCTG  
AAATATCAGAAATTTTCAATGGCTATACACTATGACCATGTAGTCAGTAATTATAT  
CATTTGGACCTTTTGAAATATTTTCAATATGTAAAGTTTTGCACCTGGAAAGGTC  
TTTTGGAGTTAAATATTTAGTATGTTATGTTTTGCATACAAGTTATAGAATGCTGTC  
35 TTCTTTTGTGCCACATCAATGGTGGGGGCAGAAATATTGTTTTGGTCAATGTA  
ATTATGACCTGCATTAGTGCTATAGTGATTGCATTTTCAGCGTGGAATGTTTAACTC  
GCAACAGAAAGTGTTGATCGACTAATAAAGATTTGCATGGCACAAAAA  
AAAAAAGTACTCTGCGTTGTTACTCGAG (SEQ ID NO:344)

40 **Translation:**

MRCLPVLII LLLLTASAPGVVVL PKTEDDVPMSVYGNK SILRGILRNGVCCGYKLCHP  
C (SEQ ID NO:345)

**Toxin Sequence:**

45 Asn-Gly-Val-Cys-Cys-Gly-Xaa5-Lys-Leu-Cys-His-Xaa3-Cys-^ (SEQ ID NO:346)

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**Name:** Mr1.2  
**Species:** marmoreus  
**Isolated:** Yes

5 **Toxin Sequence:**

Gly-Val-Cys-Cys-Gly-Xaa5-Lys-Leu-Cys-His-Xaa3-Cys-<sup>^</sup> (SEQ ID NO:347)

**Name:** Bn1.5  
**Species:** bandanus  
**Cloned:** Yes

**DNA Sequence:**

ATGCGCTGTCTCCAGTCTTGATCATTCTTCTGCTGCTGACTGCATCTGCACCTGGCG  
 TTGATGTCTTACCGAAGACCGAAGATGATGTGCCCTGTCACTGTCTACGATAATA  
 CAAAGAGTATCCTACGAGGACTTCTGGACAAACGTGCTTGTGTGGCTACAAGCTTT  
 GCTCACCATGTTAACCAGCATGAAGGATCC (SEQ ID NO:348)

**Translation:**

MRCLPVLILLLLTASAPGVDVLPKTEDDVPLSSVYDNTKSILRGLLDKRACCGYKLCSP  
 C (SEQ ID NO:349)

**Toxin Sequence:**

Ala-Cys-Cys-Gly-Xaa5-Lys-Leu-Cys-Ser-Xaa3-Cys-<sup>^</sup> (SEQ ID NO:350)

**Name:** Au1.4  
**Species:** aulicus  
**Cloned:** Yes

**DNA Sequence:**

GGAAGCTGACTACAAGCAGAATGCGCTGTCTCCAGTCTTCGTCACTTCTTGCTGC  
 TGACTGCATCTGGACCTAGCGTTGATGCCCCGACTGAAGACCAAAGATGATGTGCC  
 CTGTCACTTTTCCGAGATAATGCAAAGAGTACCTACAAAGACATCAGGACAAAAG  
 CGTTTGCTGTGGCTATAAGCTGTGTTTCCCTTGTGGTTAACCAGCATGAAGG (SEQ ID  
 NO:351)

**Translation:**

MRCLPVFVILLLLTASGPSVDARLKTDDVPLSSFRDPAKSTLQRHQDKSVCCGYKLCF  
 PCG (SEQ ID NO:352)

**Toxin Sequence:**

Ser-Val-Cys-Cys-Gly-Xaa5-Lys-Leu-Cys-Phe-Xaa3-Cys-# (SEQ ID NO:353)

**Name:** Tx1.7  
**Species:** textile

10072602.021102

**Cloned:** Yes

**DNA Sequence:**

CAGGATCCAATGGGGTTTGTGTGGCTATAGGATGTGTGTTCCCTGTGGTTAACCAG  
CATGAAGGGAATGACTTTGGATGAGACCCCTGCGAACTGTCCCTGGATGTGAGAT  
TTGGAAGCAGACTGTTCAATTTGCACGTGTTCTGTGAATTTCAATGGTCGTTAAC  
AACACGCTGCCACTTGCAAGCTACTATCTCTCTGTCTTTTATCTGTGGAACGTATG  
ATCTAACAACTGAAATATCATANANATTTTCAATGGGTATNCACTATGCATATGAT  
CATGTAGGGTTC AAGGGTCAAGATNC (SEQ ID NO:354)

**Translation:**

GSNGVCCGYRMCVPCG (SEQ ID NO:355)

**Toxin Sequence:**

Asn-Gly-Val-Cys-Cys-Gly-Xaa5-Arg-Met-Cys-Val-Xaa3-Cys-# (SEQ ID NO:356)

**Name:** Tx1.6

**Species:** textile

**Cloned:** Yes

**DNA Sequence:**

ATGCACTGTCTCCCAATCTTCGTCAATCTTCTGCTGCTGACTGCATCTGGACCTAGCG  
TTGACTGCCCAACTGAAGACCAAAGATGATGTGCCCTGTCATCTTCCGAGATCATG  
CAAAAGAGTACCCTACGAAGACTTCAGGACAAACAGACTTGCTGTGGCTATAGGATG  
TGTGTTCTTGTGGTTAAC CAGCATGAAGGATCC (SEQ ID NO:357)

**Translation:**

MHCLPIFVILLLLTASGPSVDAQLKTKDDVPLSSFRDHAKSTLRLRLQDKQTCCGYRMCCV  
PCG (SEQ ID NO:358)

**Toxin Sequence:**

Xaa2-Thr-Cys-Cys-Gly-Xaa5-Arg-Met-Cys-Val-Xaa3-Cys-# (SEQ ID NO:359)

**Name:** Af1.3

**Species:** ammimalis

**Cloned:** Yes

**DNA Sequence:**

AGAAGCTGACTACAAGCAGAATGCACTACCTCCCAGTCTTCGTCATTCTTCTGCTGC  
TGACTGCATCTGGACCTAGCGTTGATGCCCAACTGAAGACCAAAGATGATGTGCC  
CTGTCACTTTCCGAGATAATGCAAAGAGTACCCTACGAAGACTCCAGTACAAACA  
GGCTTGCTGTGGCTTAAAGATGTGTGTTCTTGTGGTTAAC CAGCATGAAGG (SEQ  
ID NO:360)

**Translation:**

10072602-021402

MHYLPVFVILLLLTASGPSVDAQLKTKDDVPLSSFRDnakSTLRLRLQYKQACCGFKMC  
VPCG (SEQ ID NO:361)

**Toxin Sequence:**

5 Xaa2-Ala-Cys-Cys-Gly-Phe-Lys-Met-Cys-Val-Xaa3-Cys-# (SEQ ID NO:362)

**Name:** Pn1.3  
**Species:** pennaceus  
**Cloned:** Yes

**DNA Sequence:**

ATGCGCTGTCTCCAGTCTTCGTCATTCTTCTGCTGCTGACTGCATCTGCACCTAGCG  
TTGATGCCAAAGTTCATCTGAAGACCAAAGGTGATGGGCCCTGTCATCTTTCCGAG  
ATAATGCAAAAGAGTACCCTACAAAGACTTCAGGACAAAAGCACTTGCTGTGGCTTT  
AAGATGTGTATTCTTGTGCTTAACCAGCATGAAGGATCC (SEQ ID NO:363)

**Translation:**

MRCLPVFVILLLLTASAPSVDaKVHLKTKGDGPLSSFRDnakSTLQRLQDKSTCCGFKM  
CIPCR (SEQ ID NO:364)

**Toxin Sequence:**

Ser-Thr-Cys-Cys-Gly-Phe-Lys-Met-Cys-Ile-Xaa3-Cys-Arg-^ (SEQ ID NO:365)

**Name:** Pn1.4  
**Species:** pennaceus  
**Cloned:** Yes

**DNA Sequence:**

CAGGATCCAATGGGGTTTGTGTGGCTTTTGGATGTGTATTCTTGTAAATTAACCAG  
CATGAAGGGAAATGACTTTGGATAAGACCCCTGCGAACTGTCCTTGGATGTGAGAT  
TTGGAAAGCAGACTGTTCTTTTGCACGTGTCGTGGAATTTGGAATGGTCGTTAAC  
AACACGCTGCCACTTGCAAGCTACTATCTCTGTCTTTCATCTGTGGAACGTATG  
ATCTAACAACTGAAATATCATAGAAATTTTCAATGGGTATACACTATGCATATGAC  
CATGTANGGGTCAACAGNC (SEQ ID NO:366)

**Translation:**

GSNGVCCGFWMCIPCN (SEQ ID NO:367)

**Toxin Sequence:**

Asn-Gly-Val-Cys-Cys-Gly-Phe-Xaa4-Met-Cys-Ile-Xaa3-Cys-Asn-^ (SEQ ID NO:368)

**Name:** Om1.7  
**Species:** omaria  
**Cloned:** Yes

10072607.021102

**DNA Sequence:**

GGAAGCTGACTACAAGCAGAATGCGCTGTCTCCAGTCTTCGTCATTCTTCTGCTGC  
 TGACTGCATCTGCACCTAGCGTTGATGCCCCAGCCGAAGGCCAAAGATGATGTGCCC  
 CTGTCATCTTTCCGTGATAATGCAAAGAGTACCCATACAAAGACTTCAGGACAAAGA  
 CGTTTGCTGTTACGTTAGAATGTGTCCTTGTCGTTAACAGCATGAAGG (SEQ ID  
 NO:369)

**Translation:**

MRCLPVFVILLLLTASAPSVDARPKAKDDVPLSSFRDPAKSTLQRLQDKDVCCYVRMC  
 PCR (SEQ ID NO:370)

**Toxin Sequence:**

Asp-Val-Cys-Cys-Xaa5-Val-Arg-Met-Cys-Xaa3-Cys-Arg-<sup>^</sup> (SEQ ID NO:371)

**Name:** Conophysin-R

**Species:** radiatus

**Isolated:** Yes

**Toxin Sequence:**

His-Xaa3-Thr-Lys-Xaa3-Cys-Met-Xaa5-Cys-Ser-Phe-Gly-Gln-Cys-Val-Gly-Xaa3-His-Ile-Cys-  
 Cys-Gly-Xaa3-Thr-Gly-Cys-Xaa1-Met-Gly-Thr-Ala-Xaa1-Ala-Asn-Met-Cys-Ser-Xaa1-Xaa1-  
 Asp-Xaa1-Asp-Xaa3-Ile-Xaa3-Cys-Gln-Val-Phe-Gly-Ser-Asp-Cys-Ala-Leu-Asn-Asn-Xaa3-  
 Asp-Asn-Ile-His-Gly-His-Cys-Val-Ala-Asp-Gly-Ile-Cys-Cys-Val-Asp-Asp-Thr-Cys-Thr-Thr-  
 His-Leu-Gly-Cys-Leu-<sup>^</sup> (SEQ ID NO:372)

**Name:** Ts10.1

**Species:** tessulatus

**Cloned:** Yes

**DNA Sequence:**

GGATCCATGTTACCCGTGTTTCTGTTGGTTGTCTTGCCAACCACTGTTGTTTCCTTCA  
 GTGCAGATCGTGCCAACGTCAAAGCGTCTGACCTGATCGCCAGGCCACCAGAGAC  
 GGCTGTCCACCACATCCCCTGCTGATGCATAAGTGCATGTGTACTAATACATGT  
 GGTGAAGACGCTGATGCTCCAGGACCCTCTGAACCAACGACCTCGAG (SEQ ID  
 NO:373)

**Translation:**

MFTVLLVVLATTVVFSADRANVKASDLIAQATRDGCPHPVPGMHKCMCTNTCG  
 (SEQ ID NO:374)

**Toxin Sequence:**

Asp-Gly-Cys-Xaa3-Xaa3-His-Xaa3-Val-Xaa3-Gly-Met-His-Lys-Cys-Met-Cys-Thr-Asn-Thr-  
 Cys-# (SEQ ID NO:375)

10072602.021202

**Name:** G1.4  
**Species:** geographus  
**Cloned:** Yes

**DNA Sequence:**

ANNTAGANTNTGCTGANTANNGGATCNTAANTANTGNNTCGANATGATNANGAGT  
 GATAAAATGANNGGTGCACNTNTANTTANGNTNNTANGATNNNNATATTATNNTANN  
 NNNTAANANATATNGGTTNNGGANNAAAGAGANTAAAAGTANNGNTTNGTGAAANA  
 ANGANNNNATGTTNNANNTCATAACNNNAATGTAATAATANACGNNCCAGTGTG  
 AAANNNTNTCNNNNATAAAAAATTCTNTNTNTNAANGTNNNTGTNTGNGTGTGTGTG  
 TGTGTGTGTGTGTGTGNGTGTGTGNGTGTGTGTGTGTGTGTGTGTGTGTGNGTGT  
 GTGTNTGTGNGT  
 CCAGCATCTGATGNCAGGGATGACACAGCCAAAGACGAAGGGTCTNACATGGACA  
 AATTGGTCGAGAAAAAAGAATGTTGCCATCTGCCTGTGGCAAAACACTACAGTTGT  
 GGACGCTGATGCTCCAGGGTNTGAAGGANCAA (SEQ ID NO:376)

**Translation:**

SDXRDDTAKDEGSXMDKLVEKKECHPACGKHYSGR (SEQ ID NO:377)

**Toxin Sequence:**

Xaa1-Cys-Cys-His-Xaa3-Ala-Cys-Gly-Lys-His-Xaa5-Ser-Cys-# (SEQ ID NO:378)

**Name:** G1.5  
**Species:** geographus  
**Cloned:** Yes

**DNA Sequence:**

GGATCCATGTTACCCGTGTTTCTGTTGGTGGTCTTGCGCAACCACTGTCGTTTCCTTCC  
 CTTGAGAACGTGCATCTGATGGCAGGGATGACACAGCCAAAGACGAAGGGTCTGAC  
 ATGGAGAAATTGGTCGAGAAAAAAGAATGTTGCAATCTGCCTGTGGCAGACACTT  
 CAGTTTGTGGACGCTGATGCTCCAGGACCTCTGAACCACGACTCGAG (SEQ ID  
 NO:379)

**Translation:**

MFTVFLVVLATTVVSFPERASDGRDDTAKDEGSDMEKLVEKKECCNPACGRHFSCG  
 R (SEQ ID NO:380)

**Toxin Sequence:**

Xaa1-Cys-Cys-Asn-Xaa3-Ala-Cys-Gly-Arg-His-Phe-Ser-Cys-# (SEQ ID NO:381)

**Name:** S1.8  
**Species:** striatus  
**Cloned:** Yes

**DNA Sequence:**

GGATCCATGTTACCGTGTCTTCTGTTGGTTGTCTTGGCAACCACTGTCGTTTCCTTCA  
 CTTCAGATCGTGCATCTGATGGCAGGGATGACGAAGCCAAAGACGAAAGGTCTGAC  
 ATGCACGAATCGGACCGGAAAGGACGCGCATACTGTTGCCATCCTGCCTGTGGCCC  
 AAATATAGTTGTGGCACCTCATGCTCCAGGACCTCTGAACCACGACCTCGAG  
 (SEQ ID NO:382)

**Translation:**

MFTVFLLVLLATTVVSFTSDRASDGRDDEAKDERSDMHESDRKGRAYCCHPACGPNY  
 SCGTSCSRTL (SEQ ID NO:383)

**Toxin Sequence:**

Ala-Xaa5-Cys-Cys-His-Xaa3-Ala-Cys-Gly-Xaa3-Asn-Xaa5-Ser-Cys-Gly-Thr-Ser-Cys-Ser-Arg-  
 Thr-Leu-^ (SEQ ID NO:384)

**Name:** S1.9  
**Species:** striatus  
**Cloned:** Yes

**DNA Sequence:**

GGATCCATGTTACCGTGTCTTCTGTTGGTTGTCTTGGCAACCACTGTCGTTTCCTTCA  
 CTTCAGATCGTGCATCTGATGGCAGGGATGACGAAGCCAAAGACGAAAGGTCTGAC  
 ATGCACGAATCGGACCGGAAAGGACGCGCATACTGTTGCCATCCTGTCTGTGGCAA  
 AAATTTGATTGTGGACGCTGATGCTCCAGGACCTCTGAACCACGACCTCGAG  
 (SEQ ID NO:385)

**Translation:**

MFTVFLLVLLATTVVSFTSDRASDGRDDEAKDERSDMHESDRKGRAYCCHPVCCKNF  
 DCGR (SEQ ID NO:386)

**Toxin Sequence:**

Ala-Xaa5-Cys-Cys-His-Xaa3-Val-Cys-Gly-Lys-Asn-Phe-Asp-Cys-# (SEQ ID NO:387)

**Name:** Ra1.1  
**Species:** rattus  
**Cloned:** Yes

**DNA Sequence:**

GGATCCATGTTACCGTGTCTTCTGTTGGTTGTCTTGGCAACCACTGTCGTTTCCTTCC  
 CTTCAGATCGTGCATCTGATGGCAGGGATGACGAAGCCAAAGACGAAAGGTCTGAC  
 ATGCACGAATCGGACCGGAATGGACGCGGATGCTGTTGCAATCCTGCCTGTGGCCC  
 AAATATGGTTGTGGCACCTCATGCTCCAGGACCTCTGAACCACGACCTCGAG  
 (SEQ ID NO:388)

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**Translation:**

MFTVFLLVVLATTVVSFSPDRASDGRDDEAKDERSDMHESDRNGRGCCCNPACGPNY  
GCGTSCSRTL (SEQ ID NO:389)

**Toxin Sequence:**

Gly-Cys-Cys-Cys-Asn-Xaa3-Ala-Cys-Gly-Xaa3-Asn-Xaa5-Gly-Cys-Gly-Thr-Ser-Cys-Ser-Arg-  
Thr-Leu-<sup>^</sup> (SEQ ID NO:390)

**Name:** Ar1.1  
**Species:** arenatus  
**Cloned:** Yes

**DNA Sequence:**

GGATCCATGTTACCGTGTCTTCTGTTGGTTGTCTTGGCAACCACTGTGGATTCCTTCA  
CTCCAGTTCGTACTTCTGTGTCAGGAGTGCTGCAGCCAACGCGTTTGACCGGATCG  
CTCTGACCGCCAGGCAAGATTATTGCTGTACCATTCCCAGCTGTTGGGATCGCTATA  
AAGAGAGATGTAGACACATACGCTGATGCTCCAGGACCTCTGAACCACGACCTTG  
AG (SEQ ID NO:391)

**Translation:**

MFTVFLLVVLATTVDSTFPVRTSVGRSAAANAFDRIALTARQDYCCTIPSCWDYKERC  
RHIR (SEQ ID NO:392)

**Toxin Sequence:**

Xaa2-Asp-Xaa5-Cys-Cys-Thr-Ile-Xaa3-Ser-Cys-Xaa4-Asp-Arg-Xaa5-Lys-Xaa1-Arg-Cys-Arg-  
His-Ile-Arg-<sup>^</sup> (SEQ ID NO:393)

**Name:** Er1.1  
**Species:** eburneus  
**Cloned:** Yes

**DNA Sequence:**

GGATCCATGTTACCGTGTCTTCTGTTGGTTGTCTTGGCAACCACTGTGGATTCCTTCA  
CTTCAGTTCGTACTTCCGTTGGCAGGAGTGCTGCAGCCAACGCGTTTGACCGGATCG  
CTCTGACCGCCAGGCAAGATTATTGCTGTACCATTCCCAGCTGTTGGGATCGCTATA  
AAGAGAGATGTAGACACATACGCTGATGCTCCAGGACCTCTGAACCACGACCTCG  
AG (SEQ ID NO:394)

**Translation:**

MFTVFLLVVLATTVDSTSVRTSVGRSAAANAFDRIALTARQDYCCTIPSCWDYKERC  
RHIR (SEQ ID NO:395)

**Toxin Sequence:**

Xaa2-Asp-Xaa5-Cys-Cys-Thr-Ile-Xaa3-Ser-Cys-Xaa4-Asp-Arg-Xaa5-Lys-Xaa1-Arg-Cys-Arg-His-Ile-Arg-^ (SEQ ID NO:396)

5 **Name:** Mil.2  
**Species:** miles  
**Cloned:** Yes

**DNA Sequence:**

10 GGATCCATGTTACCGTGTTTCTGTTGGTTGCTTTGGCAACTGCTGTTCTTCCAGTCA  
 CTTTAGATCGTGCATCTGATGGAAGGAATGCAGCAGCCAACGCCAAAACGCCTCGC  
 CTGATCGCGCCATTTCATCAGGGATTATTGCTGTCATAGAGGTCCCTGTATGGTATGG  
 TGTGGTTGAAGCCGCTGCTGCTCCAGGACCCTCTGAACCACGACCTCGAG (SEQ ID  
 NO:397)

**Translation:**

MFTVFLLVLATAVLPVTLDRASDGRNAAANAKTPRLIAPFIRDYCCHRGPCMVWCG  
 (SEQ ID NO:398)

**Toxin Sequence:**

Asp-Xaa5-Cys-Cys-His-Arg-Gly-Xaa3-Cys-Met-Val-Xaa4-Cys-# (SEQ ID NO:399)

**Name:** Jp1.1  
**Species:** jaspadius  
**Cloned:** Yes

**DNA Sequence:**

30 GGATCCATGTTACCGTGTTTCTGTTGGTTGCTTTGGCAACCACTGTCGTTTCCAACCT  
 CTTTCAAGATCGTGGTCCAGCATCTAATAAAAGGAAGAATGCCGCAATGCTTGACATG  
 ATCGCTCAACACGCCATAAGGGGTTGCTGTTCCGATCCTCGCTGTAGATATAGATGT  
 CGTTGAAGACGCTGCTGCTCCAGGACCCTCTGAACCACGACCTCGAG (SEQ ID  
 NO:400)

**Translation:**

MFTVFLLVLATTVVSNSSDRGPASNKRKNAAMLDMIAQHAIRGCCSDPRCRYRCR  
 (SEQ ID NO:401)

**Toxin Sequence:**

40 Gly-Cys-Cys-Ser-Asp-Xaa3-Arg-Cys-Arg-Xaa5-Arg-Cys-Arg-^ (SEQ ID NO:402)

**Name:** a-OmIA  
**Species:** omaria  
**Isolated:** Yes

**Toxin Sequence:**

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Gly-Cys-Cys-Ser-His-Xaa3-Ala-Cys-Asn-Val-Asn-Asn-Xaa3-His-Ile-Cys-Gly-# (SEQ ID NO:403)

5 **Name:** a-OmIA [COOH]  
**Species:** omaria  
**Cloned:** No

**Toxin Sequence:**

10 Gly-Cys-Cys-Ser-His-Xaa3-Ala-Cys-Asn-Val-Asn-Asn-Xaa3-His-Ile-Cys-Gly-^ (SEQ ID NO:404)

**Name:** Qc1.1  
**Species:** quercinus  
**Cloned:** Yes

**DNA Sequence:**

GGATCCATGTTACCGTGTGTTCTGTTGGTTGTCTTGCCAACCACTGTCACCTTCAGATC  
 GTGTATCTAATGGCAGGAAAGCTGCAGCCAAATTCAAAGCGCCTGCCCTGATGGAG  
 CTGTCCGTCAGGCAAGGATGCTGTTCAGATCCTGCCTGTGCCGTGAGCAATCCAGAC  
 ATCTGTGGCGGAGGACGCTGATGCTCCAGGACCTCTGAACCACGACCTCGAG (SEQ ID NO:405)

**Translation:**

MFTVFLLVVLATTVTS DRVSNRKA AAKFKAPALMELSVRQGCCSDPACAVSNPDICG  
 GGR (SEQ ID NO:406)

**Toxin Sequence:**

30 Xaa2-Gly-Cys-Cys-Ser-Asp-Xaa3-Ala-Cys-Ala-Val-Ser-Asn-Xaa3-Asp-Ile-Cys-Gly-Gly-#  
 (SEQ ID NO:407)

**Name:** Bn1.6  
**Species:** bandanus  
**Cloned:** Yes

**DNA Sequence:**

GGATCCATGTTACCGTGTGTTCTGTTGGTTGTCTTGCCAACCACTGTTGTTTCCTTCA  
 CTTCAAATCGTGCAATTCGTCGTAGGAATGCCGTAGCCAAAGCGTCTGACCTGATCG  
 CTCTGAACGCCAGGAGACCAGAATGCTGTACTCATCTGCTGTACGTGAGTCATC  
 CAGAACTCTGTGGTTGAAGACGCTGACGCTCCAGGACCTCTGAACCACGACCTCG  
 AG (SEQ ID NO:408)

**Translation:**

MFTVFLLVVLATTVV SFTSNRAFRRRNAVAKASDLIALNARRPECCTHPACHVSHPELC  
 G (SEQ ID NO:409)

10075602.02102  
 2012.02.22

**Toxin Sequence:**

Xaa3-Xaa1-Cys-Cys-Thr-His-Xaa3-Ala-Cys-His-Val-Ser-His-Xaa3-Xaa1-Leu-Cys-# (SEQ ID NO:410)

**Name:** Mr1.5  
**Species:** marmoreus  
**Cloned:** Yes

**DNA Sequence:**

GGATCCCATGTTACCCGTGTTTCTGTGTGGTTGTCTTGGAACCACTGTTGTTTCCTTCA  
 CTTCAAATCGTGTTCTGGATCCAGCATTTCTGTCGTAGGAATGCCGCAGCCAAAGCGT  
 CTGACCTGATCGCTCTGAACGCCAGGAGACCAGAATGCTGTACTCATCCTGCCTGTC  
 ACGTGAGTAATCCAGAACTCTGTGGCTGAAGACGCTGATGCTCCAGGACCCTCTGA  
 ACCACGACCTCGAG (SEQ ID NO:411)

**Translation:**

MFTVFLLVVLATTVVSFTSNRVLDPAFRRRNAAKASDLIALNARRPECCTHPACHVSN  
 PELCG (SEQ ID NO:412)

**Toxin Sequence:**

Xaa3-Xaa1-Cys-Cys-Thr-His-Xaa3-Ala-Cys-His-Val-Ser-Asn-Xaa3-Xaa1-Leu-Cys-# (SEQ ID NO:413)

**Name:** Mi1.1  
**Species:** miles  
**Cloned:** Yes

**DNA Sequence:**

GGATCCCATGTTACCCGTGTTTCTGTGTGGTTGTCTTGGAACCACTGTCGTTTCCGTCA  
 CTTTCATATCGTGCATCTCATGGCAGGAAGGACGCAGCCGACCTGAGCGCTCTGAAC  
 GACAACAATAATTGCTGTAACCATCCTGCCTGTGCCGGGAAAAATTCAGATCTTTGT  
 GGTTGAAGACGCTGCTGCTCCAGGACCCTCTGAACCACGACCTCGAG (SEQ ID  
 NO:414)

**Translation:**

MFTVFLLVVLATTVVSVTSYRASHGRKDAADLSALNDNNCCNHPACAGKNSDLCG  
 (SEQ ID NO:415)

**Toxin Sequence:**

Cys-Cys-Asn-His-Xaa3-Ala-Cys-Ala-Gly-Lys-Asn-Ser-Asp-Leu-Cys-# (SEQ ID NO:416)

**Name:** MII[YHT]  
**Species:** magus

**Toxin Sequence:**

Gly-Cys-Cys-Xaa5-His-Xaa3-Thr-Cys-His-Leu-Xaa1-His-Ser-Asn-Leu-Cys-# (SEQ ID NO:417)

**Name:** Nb1.1  
**Species:** nobilis  
**Cloned:** Yes

**DNA Sequence:**

GGATCCATGTTACCGTGTTTCTGTTGGTTGTCTTGGCAACCACTGTTGTTTCCTTCA  
 CTTGAGATCGTGCATCTGATGGCAGGAATGCCGCAGCCAAAGCTTCTGACCTGATTG  
 CTTTGACCGTCAGGGGATGCTGTGAGCGACCTCCCTGTCGCTGGCAAAATCCAGATC  
 TTTGTGGTGGGAAGGCGCTGANATTCAGGACCCTCTGAACCACGACCTCGAG (SEQ  
 ID NO:418)

**Translation:**

MFTVFLLVVLATTVVSFTSDRASDGRNAAKASDLIALTVRGCCERPPCRWQNPDLGG  
 GRR (SEQ ID NO:419)

**Toxin Sequence:**

Gly-Cys-Cys-Xaa1-Arg-Xaa3-Xaa3-Cys-Arg-Xaa4-Gln-Asn-Xaa3-Asp-Leu-Cys-Gly-# (SEQ ID NO:420)

**Name:** Ak1.1  
**Species:** atlanticus  
**Cloned:** Yes

**DNA Sequence:**

GGATCCATGTTACCGTGTTTCTGTTGGTTGTCTTGGCAACCACAGTCGTTTCCTTCA  
 CTTGAGATAGTGCATTGATAGCAGGAATGTCGCAGCCAACGACAAAAGTGTCTGAC  
 ATGATCGCTCTGACCGCCAGGAGAACATGCTGTTCCCGTCTACCTGTAGAATGGAA  
 TATCCAGAACTTTGTGGTGGAAGACGCTGATACTCCAGGACCCTCTGAACCACGAC  
 CTCGAG (SEQ ID NO:421)

**Translation:**

MFTVFLLVVLATTVVSFTSDSAFDSRNVAANDKVSMDIALTARRTCCSRPTCRMEYPEL  
 CGGRR (SEQ ID NO:422)

**Toxin Sequence:**

Thr-Cys-Cys-Ser-Arg-Xaa3-Thr-Cys-Arg-Met-Xaa1-Xaa5-Xaa3-Xaa1-Leu-Cys-Gly-# (SEQ ID NO:423)

**Name:** Qc1.2

**Species:** quercinus  
**Cloned:** Yes

**DNA Sequence:**

GGATCCATGTTACACCGTGTTTCTGTGTGGTTGCTTTGGCAATCACGGTGGTTTCCTTCA  
 CCTCAGATCATGCATCTGATGGCAGGAATACCGCAGCCAACGACAAAGCGTCTAAA  
 CTGATGGCTCTTACGAACGAATGCTGTGACAATCCTCCGTGCAAGTCGAGTAATCCA  
 GATTGTGTGACTGGAGAAGCTGATGCTCCAGGACCCTNTGAACCACGACCTCGAG  
 (SEQ ID NO:424)

**Translation:**

MFTVFLLVVLAITVVSFTSDHASDGRNTAANDKASKLMALTNECCDNPPCKSSNPDLCDWRS (SEQ ID NO:425)

**Toxin Sequence:**

Asn-Xaa1-Cys-Cys-Asp-Asn-Xaa3-Xaa3-Cys-Lys-Ser-Ser-Asn-Xaa3-Asp-Leu-Cys-Asp-Xaa4-Arg-Ser-^ (SEQ ID NO:426)

**Name:** Lp1.1  
**Species:** leopardus  
**Cloned:** Yes

**DNA Sequence:**

GGATCCATGTTACACCGTGTTTCTGTGTGGTTGCTTTGGCAACCACGGTCGTTTCCCTCA  
 CTTTAGATCGTGCATCTGGTGGCAGGAGATCTGGAGCCGACAACATGATTGCTCTTC  
 TGATCATCAGAAAATGCTGTTCCAATCCCGCCTGTAACAGGTATAATCCAGCAATTT  
 GTGATTGAAGACGCTAATGCTCCAGGACCCTCTGAACCACGACCTCGAG (SEQ ID  
 NO:427)

**Translation:**

MFTVFLLVVLATTVLSLTLDRASGGRRSGADNMIALLIIRKCCSNPACNRYNPAICD (SEQ ID NO:428)

**Toxin Sequence:**

Cys-Cys-Ser-Asn-Xaa3-Ala-Cys-Asn-Arg-Xaa5-Asn-Xaa3-Ala-Ile-Cys-Asp-^ (SEQ ID  
 NO:429)

**Name:** Em1.1  
**Species:** emaciatus  
**Cloned:** Yes

**DNA Sequence:**

GGATCCATGTTACACCGTGTTTCTGTGTGGTTGCTTTGGCAACCACACTGTCACTTTACATC  
 GTGCATCTAATGGCAGGAATGCCGACGCCAGCAGGAAAGCGTCTGCCCTGATCGCT  
 CAGATCGCCGCTAGAGACTGCTGTAACCTTCTGCTTGTGCCGCGAGTAATCCAGGC

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CTTTGTACTTGAAGACGCTGCTGCTCCAGGACCCTCTGAACCACGACCTCGAG (SEQ ID NO:430)

**Translation:**

5 MFTVFLLVLLATTVTLHRASNGRNAAASRKASALIAQIAGRDCNFPACAASNPGGLCT (SEQ ID NO:431)

**Toxin Sequence:**

10 Asp-Cys-Cys-Asn-Phe-Xaa3-Ala-Cys-Ala-Ala-Ser-Asn-Xaa3-Gly-Leu-Cys-Thr-^ (SEQ ID NO:432)

**Name:** C. victor alpha

**Species:** victor

**Cloned:** Yes

**DNA Sequence:**

GGATCCATGTTACCGTGTTTCTGTTGGTTGCTCTTGCCAACCAACCATCGTTTCCTCCA  
CTTTAGATCGTGCATCTGATGGCATGAATGCTGCAGCGTCTGACCTGATCGCTCTGA  
GCATCAGGAGATGCTGTTCTTCTCCTCCCTGTTTCGCGAGTAATCCAGCTTGTGGTA  
GACGACGCTGATGCTCCAGGACCCTCTGAACCACGACCTCGAG (SEQ ID NO:433)

**Translation:**

5 MFTVFLLVVLATTIVSSTLDRASDGMNAAASDLIALSIRRCSSPPCFASNPACGRRR (SEQ ID NO:434)

**Toxin Sequence:**

Cys-Cys-Ser-Ser-Xaa3-Xaa3-Cys-Phe-Ala-Ser-Asn-Xaa3-Ala-Cys-# (SEQ ID NO:435)

**Name:** Cj1.1

**Species:** cinereus gubba

**Cloned:** Yes

**DNA Sequence:**

35 GGATCCATGTTACCGTGTTTCTGTTGGTTGCTCTTGCCAACCACTATCGTTTCCTCCA  
CTTCAGGTCATGCATTGATGGCAGGAATGCTGCAGCCGACTACAAAGGGTCTGAA  
TTGCTTGCTATGACCGTCAGGGGAGGATGCTGTTCTTCTCCTGTATCGAAAT  
AATCCTTTTTGTGCTGGAAGACGCTGATGCTCCAGGACCCTCTGAACCACGACCTCG  
40 AG (SEQ ID NO:436)

**Translation:**

45 MFTVFLLVVLATTIVSSTSGHAFDGRNAAADYKGSELLAMTVRGGCCSFPPCIANNPFC  
AGRR (SEQ ID NO:437)

**Toxin Sequence:**

Gly-Gly-Cys-Cys-Ser-Phe-Xaa3-Xaa3-Cys-Ile-Ala-Asn-Asn-Xaa3-Phe-Cys-Ala-# (SEQ ID NO:438)

5 **Name:** Fd1.1  
**Species:** flavidus  
**Cloned:** Yes

**DNA Sequence:**

10 GGATCCATGTTACACCGTGTCTGTGGTTGTCTTCGCATCCTCTGTCACTTTAGATC  
 GTGCATCTCATGGCAGGTATATCCAGTCGTCGACAGAGCGTCTGCCCTGATGGCTC  
 AGGCCGACCTTAGAGGTTGCTGTCCAATCCTCCTTGTCTTATCTTAATCCAGCCTG  
 TGGTTAAAGACGCTGCCGCTCCAGGACCCTCTGAACCACGACCTCGAG (SEQ ID NO:439)

**Translation:**

MFTVFLLVVFASSVTLDRAHGRYIPVVDRAALMAQADLRGCCSNPPCSYLNPAAG  
 (SEQ ID NO:440)

**Toxin Sequence:**

Gly-Cys-Cys-Ser-Asn-Xaa3-Xaa3-Cys-Ser-Xaa5-Leu-Asn-Xaa3-Ala-Cys-# (SEQ ID NO:441)

5 **Name:** Em1.2  
**Species:** emaciatus  
**Cloned:** Yes

**DNA Sequence:**

30 GGATCCATGTTACACCGTGTCTGTGGTTGTCTTCGCATCCTCTGTCACTTTAGATC  
 GTGCATCTCATGGCAGGTATGCCGACGTCGTCACAGAGCGTCTGCCCTGATGGCTC  
 ATGCCGCCCTTCGAGATTGCTGTTCGATCCTCCTTGTGCTCATAATAATCCAGACT  
 GTCGTTAAAGACGCTGCTGCTCCAGGACCCTCTGAACCACGACCTCGAG (SEQ ID NO:442)

**Translation:**

35 MFTVFLLVVFASSVTLDRAHGRYAAVVNRASALMAHAALRDCCSDPPCAHNNPDCR  
 (SEQ ID NO:443)

**Toxin Sequence:**

40 Asp-Cys-Cys-Ser-Asp-Xaa3-Xaa3-Cys-Ala-His-Asn-Asn-Xaa3-Asp-Cys-Arg-^ (SEQ ID NO:444)

45 **Name:** Ge1.1  
**Species:** generalis  
**Cloned:** Yes

100726600.021202

**DNA Sequence:**

GGATCCATGTTACCGTGTTCCTGTTGGTTGCTCTTGCCAACACTACTGTCGTTTCCTTCA  
 CTTCAGATCGTGGGTCTGATGGCAGGAATGCCGCAGCCAAGGACAAAGCGTCTGAC  
 CTGGTCGCTCTGACCGTCAAGGGATGCTGTTCTAATCCTCCCTGTTACGCGAATAAT  
 CAAGCCTATTGTAATGGAAGACGCTGATGCTCCAGGACCCTCTGAACACGACCTC  
 GAG (SEQ ID NO:445)

**Translation:**

MFTVFLLVVLATTVVSFTSDRGSDGRNAAAKDKASDLVALT VKGCCSNPPCYANNQA  
 YCNGRR (SEQ ID NO:446)

**Toxin Sequence:**

Gly-Cys-Cys-Ser-Asn-Xaa3-Xaa3-Cys-Xaa5-Ala-Asn-Asn-Gln-Ala-Xaa5-Cys-Asn-# (SEQ ID  
 NO:447)

**Name:** Wil.1  
**Species:** wittigi  
**Cloned:** Yes

**DNA Sequence:**

GGATCCATGTTACCGTGTTCCTGTTGGTTGCTTGCCAACCACTGTCGTTTCCCCCA  
 CTAGAGATCGTGCATCTGGTGTGAGGAATGTTGTTGCAACAAGCTTTACAGACTCTGA  
 CCCACGATGAATGCTGTGCACACCCTTCCTGTTGGAAGGCCGAAGACCTGATTGTA  
 CTAATCAACGTCGCAGGACCCTCTGAACCAACGACCTCGAG (SEQ ID NO:448)

**Translation:**

MFTVFLLVVLATTVVSPTDRASGVRNVVATSFQTLTHDECCAHPSCWKAEDLICITNQ  
 RRRTL (SEQ ID NO:449)

**Toxin Sequence:**

Asp-Xaa1-Cys-Cys-Ala-His-Xaa3-Ser-Cys-Xaa4-Lys-Ala-Xaa1-Asp-Leu-Ile-Cys-Thr-Asn-Gln-  
 Arg-Arg-Arg-Thr-Leu-^ (SEQ ID NO:450)

**Name:** Cal.5  
**Species:** characteristicus  
**Cloned:** Yes

**DNA Sequence:**

GGATCCATGTTACCGTGTTCCTGTTGGTTGCTCTTGCCAACCACTGTCGTTTCCTTCA  
 CTTAGATCGTGCCTGTAAGGCAGGAATGCTGCAGCCAAGGACAAAGCGTCTGAC  
 CTGGTGGCTCTGAGAGTCAGGGGATGCTGTGCCATTGCTGAATGTCGCTTGCAGAAT  
 GCAGCGTATTGTTGGTGAATATCCTGATGCTCCAGGACCCTCTGAACCAACGACCTCG  
 AG (SEQ ID NO:451)

15072502.021102

**Translation:**

MFTVFLLVLATTVVSFTSDRASEGRNAAAKDKASDLVALRVRGCCAIRECRLQNAAY  
CGGIS (SEQ ID NO:452)

**Toxin Sequence:**

Gly-Cys-Cys-Ala-Ile-Arg-Xaa1-Cys-Arg-Leu-Gln-Asn-Ala-Ala-Xaa5-Cys-Gly-Gly-Ile-Ser-  
(SEQ ID NO:453)

Name: Bt1.10  
Species: betulinus  
Cloned: Yes

**DNA Sequence:**

AGTAATTNATATANNAGAAAGNAANANAAAAANNATANAGAAATTTAAGTAATNTAA  
GAANNAGAGANAGTGAATAGNAGNTAAGTAGANNAAGANAGGTAGANAGNANANG  
NGGANGNTAGNTAATAGATANNNTATNGAGANATTANTAGCNGTATANANAAGAA  
AAGAGGGNAANNGAAATGNNGNAANNATAANTANTANNATNGANNNGNAAGTG  
NNAAGNGTANAAGGAANAACAAANTNGTTGTNTAATNTGNNTGNGTGTGINTGTGT  
GNGTGTGTGTGTGTGNGTGTGTNTGTGNGNNTGTGTGNGNGNGNGNGTGTGT  
GTGTGNGT  
TCCAGCATCTGGTGGCAGGAAGGCTGCAGCCAAAGCGTCTAACC GGATCGCTCTGA  
CCGTCAGGAGTGCAACATGCTGTTATTATCCTCCCTGTTACGAGGCTTATCCAGAAA  
GTTGTCTGTAAACGTGAATCATCCAGACCTTTGTGGCTGAAGACCCTGATGCTCCAGG  
GCAGAGTTCAA (SEQ ID NO:454)

**Translation:**

SGGRKAAAKASNRIALTVR SATCCYYPPEAYPESCL (SEQ ID NO:455)

**Toxin Sequence:**

Ser-Ala-Thr-Cys-Cys-Xaa5-Xaa5-Xaa3-Xaa3-Cys-Xaa5-Xaa1-Ala-Xaa5-Xaa3-Xaa1-Ser-Cys-  
Leu-<sup>^</sup> (SEQ ID NO:456)

**Where:**

Xaa1 is Glu or  $\gamma$ -carboxy-Glu

Xaa2 is Gln or pyro-Glu

Xaa3 is Pro or hydroxy-Pro

Xaa4 is Trp (D or L) or bromo-Trp (D or L)

Xaa5 is Tyr, <sup>125</sup>I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<sup>^</sup> is free carboxyl or amidated C-terminus, preferably free carboxyl

# is free carboxyl or amidated C-terminus, preferably amidated

? is free carboxyl or amidated C-terminus

10725602.021102

TABLE 2Alignment of  $\gamma$ -Conopeptides<sup>1</sup> (SEQ ID NO:)

4/43	SNX	-----DCRGYDAPCSSGAPCCDWWTCSARTNRCF <sup>^</sup> (457)
Af6.1		GMW---GDCKDGLTT <sup>^</sup> CFAPSECCSE-DC-E-GS-CTMW <sup>^</sup> (458)
5	Af6.2	---WREGSCTSWLATCTQDQCC <sup>^</sup> CTD-VCYKRDY-CALWDDR <sup>^</sup> (459)
Af6.3		-----N---CSDDWQYCESPSDCSSW-DC-D-VV-CS <sup>^</sup> (460)
Af6.4		--WWRWGGCMAWFGKCSKDSECCSN-SC-DITR-CELMRFPDPW <sup>^</sup> (461)
Af6.5		-----DCRGYDAPCSSGAPCCDWWTCSARTGRCF <sup>^</sup> (462)
Af6.6		---L---CPDYTEPCSHAHECCSW-NC-HNGH-CT <sup>^</sup> # (463)
10	Af6.7	-----CSSWAKYCEVDSECCSE-QC-VRSY-CAMW <sup>^</sup> (464)
g-PnVIIA		-----DCTSWFGRCTVNSXCCSN-SC-DQTY-CXLYAFOS <sup>^</sup> 2 (465)
Gm6.7		-----ECRAWYAPCSPGAQCCSLLMCSKATSRCILAL <sup>^</sup> 2 (466)
J010		-----CKTYSKYCXADSCCTX-QC-VRSY-CTLF <sup>^</sup> #2 (467)
Mr6.1		-----N-GQCEDVWMPCTSNWXCCSL-DC-E-MY-CTQI <sup>^</sup> #2 (468)
15	Mr6.2	-----CGGWSTYCEVDXCCSE-SC-VRSY-CTLF <sup>^</sup> #2 (469)
Mr6.3		-----N-GGCKATWMSCSSGWXCCSM-SC-D-MY-C <sup>^</sup> #2 (470)
R6.10		--UFGHXCTYULGPCXVDDTCCSA-SC-XSKF-CGLU <sup>^</sup> (471)
R6.9		--WWE-GECSNWLGCSTPSNCCLK-SC-N-GH-CTLW <sup>^</sup> (472)
20	Tx6.1	---L---CODYTXOC SHAHXCCSW-NC-YNGH-CT <sup>^</sup> #2 (473)
Tx6.14		-----DCYSWLGSCTAPSQCCSE-VC-D-YY-CRLWR <sup>^</sup> (474)
Tx6.4		--WL---ECSVWFSHCTKDSXCCSN-SC-DQTY-CTLMPDPW <sup>^</sup> 2 (475)
Tx6.5		GMW---GECKDGLTTCLAPSXCCE-DC-E-GS-CTMW <sup>^</sup> 2 (476)
Tx6.6		D-WWD-DGCSV-WGPCTVNAXCCSG-DC-H-ET-CIFGWEV <sup>^</sup> 2 (477)
25	Tx6.9	--WWRWGGCMAWFGCLSRDSXCCSN-SC-DVTR-CELMFPDPW <sup>^</sup> 2 (478)
TxVIIA		-----CGGYSTYCXVDSXCCSD-NC-VRSY-CTLF <sup>^</sup> # (479)

<sup>1</sup> The E may be Glu or Gla, the P may be Pro or hydroxy-Pro, and W may be Trp or bromo-Trp.

<sup>2</sup> Peptide disclosed in U.S. Serial No. 09/210,952 (PCT/US98/26792).

TABLE 3Alignment of  $\sigma$ -Conopeptides (SEQ ID NO:)

Ca8.1		GCS-GT-CHRRDGGK-RGTCD <sup>^</sup> CSG-YSYCRG-DAHFFYRGCTCSCQ <sup>^</sup> # (480)
Ca8.2		GCSG-T-CHRRDGGK-RGTCD <sup>^</sup> CSG-YSYCRG-DAHFFYRGCTCTC <sup>^</sup> (481)
35	Ca8.3	GCSG-T-CRRHRDGGK-RGTCD <sup>^</sup> CSG-YSYCRG-DAHFFYRGCTCTC <sup>^</sup> (482)
Ca8.4		GCSG-T-CRRHRDGGK-RGTCD <sup>^</sup> CSG-YSYCRG-DAHFFYRGCTCTC <sup>^</sup> (483)
Ca8.5		GCSG-T-CHRRDGGK-RGTCD <sup>^</sup> CSG-YSYCRG-DAHFFYRGCTCTC <sup>^</sup> (484)
Ca8.6		GCSG-T-CHRRQNGEC-QGTCD <sup>^</sup> CDG-HDHCDG-DTLGTYS <sup>^</sup> GCVCIC <sup>^</sup> (485)
La8.1		QSE--TACRSLGSYQCM-GKQ- <sup>^</sup> LGVHSWCBCIYNRGSQKSGCACRCQK <sup>^</sup> (486)
40	Mn8.1	QCTLVNCDRNGERACIN-GDCSC <sup>^</sup> EGQI--CKCGYRVSPGKSGCACTCRNAK <sup>^</sup> (487)
P8.1		GCS-GSPCFKNKT--C-RDECICGG-LSNCWCGY-GGS--RGCKCTCRE <sup>^</sup> (488)
R8.1		KCNF-DKCKGTGVYNCG-ESCSCEGLHS-CRCTYNIGSMKSGCACTCTY <sup>^</sup> (489)
R8.2		YGLGCA-GT-CGSSN--CVRDYCD <sup>^</sup> C-P-KPNCYCT-GKGFRQPGCGCSCL <sup>^</sup> # (490)
Sx8.1		QCTFVNNCQNG--CAN-GDCSC <sup>^</sup> GDQI--CKCYRISPGRSGCACTCRNAK <sup>^</sup> (491)
45	T8.1	FGPIC--T-CFKSQN--C-RGSC <sup>^</sup> ECMS-PPGYCS-NNGIRRGCSCTCPGT <sup>^</sup> # (492)
T8.2		GCT--GNCDW---TCS-GDCSCQGTSDSCHCIPPKSIGNR-CRCQCKRKIEID <sup>^</sup> (493)

TABLE 4Alignment of  $\tau$ -Conopeptides (SEQ ID NO:)

	Tx5.2a	---ECCEDGW-CCTAAPLT# <sup>1</sup> (494)
	Tx5.2b	---GCCEDGW-CCTAAPLT# <sup>1</sup> (495)
5	Mr5.1	---NGCC-RAGDCCSRFEIKENDF# <sup>1</sup> (496)
	Mr5.3	---NGCC-RAGDCCS <sup>^</sup> (497)
	Mr5.2	---NACC-IVRQCC <sup>^</sup> (498)
	Qc5.1	---GCCAR-LTCCV# <sup>1</sup> (499)
	Qc5.2	---GCCAM-LTCCV# <sup>1</sup> (500)
10	t-PVA	---GCCPKQMRCCTL# <sup>1</sup> (501)
	Ca5.1	----CCPRRLACCII# <sup>1</sup> (502)
	Ca5.2	----CCPNK-PCCFI# <sup>1</sup> (503)
	G5.1	-ZGWCCCKENIACCI <sup>^</sup> (504)
	G5.2	-ZGWCCCKENIACCV <sup>^</sup> (505)
5	Im5.1	DWNSCCGKNPGCCPW# <sup>1</sup> (506)
	Bt5.1	---NCCPDSPPCCH <sup>^</sup> (507)
	Af5.2	---GNCCFEWFCDD <sup>^</sup> (508)
	Da5.1	----CCEYWKLC# (509)
	Om5.1	---VCCGYKFFCCR <sup>^</sup> (510)
20	t-AuVA	---FCCPVIRYCCW <sup>^</sup> (511)
	t-AuVB	---FCCPFIRYCCW <sup>^</sup> (512)
	Au5.1	----CCPMIYWCCS <sup>^</sup> (513)
	Au5.4	----CCPEIYWCCS <sup>^</sup> (514)
	Nb5.1	---ICCPILWCC# (515)
5	Af5.1	---CCPPVIWCC# (516)
	Tx5.1	----CCQTFYWCQV# <sup>1</sup> (517)
	Au5.3	WNNYCCTNELWCC# (518)
	Gm5.1	---LCCVTEWCCCEWW <sup>^</sup> (519)
	Gm5.2	---VCCRPVQDCCS# <sup>1</sup> (520)
30	Da5.2	-PVNCCPIDQSCCS <sup>^</sup> (521)
	Sf5.1	GNIHCCTKYQPCSSPS <sup>^</sup> (522)

<sup>1</sup> Peptide disclosed in U.S. Serial No. 09/497,491 (PCT/US00/03021).TABLE 5Alignment of Mar-Type Conopeptides<sup>1</sup> (SEQ ID NO:)

	Tx1.6 (Q819)	-ZTCCGYRMCVPC# (523)
	Bn1.5 (Q818)	-A-CCGYKLCSPC <sup>^</sup> (524)
	Pn1.3 (Q820)	-STCCGFKMCIPCR <sup>^</sup> (525)
40	Pn1.5 (AA200)	-STCCGFKMCIPCS <sup>^</sup> (526)
	Pn1.7 (AA456)	-STCCGFKMCIPC# (527)
	Ep1.5 (AA457)	-STCCGYRMCVPC# (528)
	Mr1.3	NGVCCGYKLCCLPC <sup>^</sup> (529)
	Pn1.6 (AA390)	--LCCGFWMCIPCN <sup>^</sup> (530)
45	Mr1.1	NGVCCGYKLCCHOC <sup>^</sup> (531)

Mr1.2	-GVCCGYKLCHOC^ (532)
Bn1.5	--ACCGYKLCSPC^ (533)
Au1.4	-SVCCGYKLCFPC# (534)
Tx1.7	NGVCCGYRMCVPC# (535)
5 Tx1.6	-ZTCCGYRMCVPC# (536)
Af1.3	-ZACCGFKMCVPC# (537)
Pn1.3	-STCCGFKMCIPCR^ (538)
Pn1.4	NGVCCGFWMCI PCN^ (539)
10 Om1.7	-DVCCYVRMC-PCR^ (540)

<sup>1</sup> Some peptides disclosed in U.S. Serial No. 09/580,201. P may also be O and O may also be P.

### TABLE 6

Alignment of Contryphans\* (SEQ ID NO:)

Contryphan-Im	Z--C-GQAWC# (541)
Contryphan-Sm-dW4, V7	GCOWQPVPC# (542)
Contryphan-Ar-1	ZYGCOOGLWCH^ (543)
C. arenatus contryphan 1A	ASGCPWRPWC# (544)
C. arenatus contryphan 2	ZYGCFVGLWCD^ (545)
C. arenatus contryphan 4	SGCPWQPCW# (546)
C. arenatus contryphan 1	SGCPWHWPWC# (547)

\* P may be Pro or hydroxy-Pro; Z may be Gln or pyro-Glu.

### TABLE 7

Alignment of  $\alpha$ A-Conopeptides\* (SEQ ID NO:)

$\alpha$ A-EIVB	GCCGKYONAAACHOCGCTVGRROOYCDROSQG# (548)
P4.1	GCCGSYPNAAACHPCGCK-DRPSYCGQ# (549)
30 P4.2	EGCC---SNPACHPCGCK-DRPSYCGQ# (550)

\* P may be Pro or hydroxy-Pro

### TABLE 8

Alignment of Bromosleeper Conopeptides\* (SEQ ID NO:)

Bromosleeper-Ar1	VVTEACEESCEEEKHCHCHVNNNGVPSCAVICW# (551)
Bromosleeper-Ar1A	IVTEACEESCEDEEKHCHCHVNNNGVPSCAVICW# (552)
Bromosleeper-Ar2	IVTEACEEHCEDEEQFCGLENGQPPCAPVCF# (553)
Bromosleeper-Ar3	VVTGACEEHCEDEEKHCCGLENGQPPCARLCL# (554)
40 Bromosleeper-Di1	NVDQECIDACQLEDKNCGRITDGEPRCAKICL# (555)
Bromosleeper-Di2	ETDQECIDICKQEDKKCCGRSNGEPTCAKICL# (556)
Bromosleeper-Di3	ETDQECIDTCEQEDKKCCGRITNGEPVCAKICF# (557)
Bromosleeper-P1	PKTEACEEVCLEEKHCCCIRSDGPKCSRKCLLSIFC^ (558)
Bromosleeper-P2	VVSECKKYCKKQKNKNCSSKHKEPRCAKICF# (559)
45 Bromosleeper-Sn	AVTEACTEDCKTQDKKCCGEMNGQHTCAKICL# (560)

Bromosleeper-T1 PKTKECERYCELEEKHCCCIRSNPKSCRICIFKFWC^ (561)  
 Bromosleeper-T2 PKTRECEMQCEQEKKHCCRVDRDTGQCAPKCLGINW^ (562)

\* The E may be Glu or Gla, the P may be Pro or hydroxy-Pro, and W may be Trp or bromo-Trp.

### TABLE 9

Alignment of Conopressins (SEQ ID NO:)

Conopressin-G CFIRNCPKG# (563)  
 Conopressin-S CIIRNCPRG# (564)

### TABLE 10

Alignment of O-Superfamily (SEQ ID NO:)

Ar6.1 -----GCTPPGGVCGYHGH---CCD-F-C---DTFNLNLSV# (565)  
 C. geogr. GS-A -----ACSGRGSRCPPO-----CCMGLTC--GREYPPRC# (566)  
 Ca6.3 (F166) -----NCGEQGEQCAT--RP--CCSLGSC-VGSRPGLLCQY# (567)  
 convulsion -----NCPY---CVVY-----CCPPAYCEASG-----CRPP# (568)  
 De6.1 -----ACKOKNNLCATIXMAX--CCSGF-CLIIY-----RC^ (569)  
 Lv6.2 (I16) -----SCGHSAGAGCYT--RP--CCPGLHC-SGGQAGGLCV^ (570)  
 Lv6.3 (I12) -----DCGESGQGCYSV-RP--CCPGLICKGTG-GGGLCRPSGI^ (571)  
 Mf6.1 (F204) -----CTPPGGLC-YHAYP--CCSKT-C---NLDTSQCEPRWS^ (572)  
 M16.2 (F162) -----CTDSDQFCNPSNHD--CCSG-KCIDDEGDNG-ICAIVPENS^ (573)  
 M16.3 (F161) -----CTEDSQFCNPSNHD--CCSG-KCIDDEGDNG-ICAIVPENS^ (574)  
 Pu6.1 (JG14) -----CSDFGSDCPVATHN--CCSG-BCFGFEDFG-LCT^ (575)  
 Qc6.4 (F025) -----ACSQVGEACFPQ-KP--CCPGFLC--NH-IGGMCHH^ (576)  
 S6.4 -----CLPDGTSCLPFRIR--CCGT--C--SSILKSCVS^ (577)  
 Ts6.3 (F081) -----SCAEFGVVC-SS-TA--CCPDLDVCEAYSP--ICLWE^ (578)  
 Tx6.3 -----KCVBQWKYCTR-----ESLCCAGL-CLFS-----FCIL^ (579)  
 Tx6.7 -----CVBQWEVCGIILFSSSCCQQL-CLFG-----FCVL^ (580)  
 Vr6.1 (F198) -----DCGGQGEQCYT--QP--CCPGLRCRGGGTGGGVQCQL^ (581)  
 Wi6.1 (M406) FGSFIPCARLGEPC-----T-ICCRPLRCRESG--TPTCQV^ (582)  
 Rg6.6 (K861) -----TCLEHNKLCWYD---RDCCIIY-C---N--ENKCGVKPQ^ (583)  
 EST202 -----ACKSNYDCPQRFKCCSYTWNGSSGYCKRVCLYR^ (584)

### TABLE 11

Alignment of  $\psi$ -Conopeptides\* (SEQ ID NO:)

$\psi$ -PIIIF GOCCCLYGSCROFOGCYNALCCRK# (585)  
 U021 homolog HPPCCMYGRCCRYPGSSASCCQ# (586)

\* P may be Pro or hydroxy-Pro

### TABLE 12

Alignment of kappaA-Conopeptides\* (SEQ ID NO:)

Cn10.3 (J454) APELVVTATTTCCGYDPMTCIPPCMCTHSCPPKRKP# (587)  
 A10.2 (H350) ZSWLVPSITTTCCGYDPGTMCPPRCRNNCTCKPKPKPGK# (588)

Cn10.4 (G851) APELVVTATTTCGGYDPMTWCPSCMCTYSCPHQRKKP# (589)  
 M10.3 (X003) APELVVTATTTCGGYDPMTCPPCMCTHSCPPKGGP# (590)  
 A10.3 (AA400) ZKWLVSHTITTCGGYNKMDMCPPCMCTYSCPLKKRP# (591)  
 A10.4 (AA401) APWTVVTATTNCCGITGPG-CLPCRCTQTC# (592)

TABLE 13

Alignment of  $\alpha$ -Conopeptides (SEQ ID NO:)

G1.4 -ECCHPACGKHYSC# (593)  
 G1.5 -ECCNPACGRHFSC# (594)  
 10 S1.8 AYCCHPACGPNYSCGTSCSRTL^ (595)  
 S1.9 AYCCHPVCGKNFDC# (596)  
 Ra1.1 GCCCNFACGPNYCGGTSCSRTL^ (597)

Ar1.1 ZDYCCITIPSCWDYRKERCRRH^ (598)  
 Er1.1 ZDYCCITIPSCWDYRKERCRRH^ (599)  
 Mi1.2 -DYCCHRGPCMVW----C# (600)  
 Jp1.1 --GCCSDPRC--RYR--CR^ (601)  
 a-OmIA --GCCSHPACNVNNPHICG# (602)  
 a-OmIA [COOH] --GCCSHPACNVNNPHICG^ (603)  
 20 Qc1.1 Z-GCCSDPACAVSNPDICGG# (604)  
 Bn1.6 PE-CCTHPACHVSHPELC# (605)  
 Mr1.5 PE-CCTHPACHVSNPELC# (606)  
 Mi1.1 ---CCNHPACAGKNSDLC# (607)  
 MII[YHT] --GCCYHPTCHLEHSNLC# (608)  
 5 Nb1.1 --GCCERPPCRWQNPDLCG# (609)  
 Ak1.1 --TCCSRPTCRMYPELCG# (610)  
 Qc1.2 NE-CCDNPPCKSSNPDLCDWRS^ (611)  
 Lp1.1 ---CCSNPACNRYNPAICD^ (612)  
 Em1.1 -D-CCNFPAACASNPGLCT^ (613)  
 30 C. victor alpha ---CCSSPPCFASNPAC# (614)  
 Cj1.1 -GGCCSFPPCIANNPF-CA# (615)  
 Fd1.1 -GCCSNPPCSYLNPA-C# (616)  
 Em1.2 -D-CCSDPPCAHNNPD-CR^ (617)  
 Ge1.1 -GCCSNPPCYANNQAYCN# (618)  
 35 Wi1.1 DE-CCAHPSCKWAEDLICTNQRRRTL^ (619)  
 Cal.5 --GCCAIRECLQNAAYCGGIS^ (620)  
 Bt1.10 SATCCYYPPCYEAYPESCL^ (621)

TABLE 14

Alignment of Conopeptides\* (SEQ ID NO:)

Convulsant VYXTHP^ (622)  
 WG002 WSWRMGNGDRRSDQ^ (623)  
 45 QcII DCQPCGHNVCC^ (624)

Scratching,  
 Convulsion KFLSGGFKXIVCHRYCAKGIKEFCNCPD# (625)

50 MAG-1 RPKNSW^ (626)

MAG-2	AROKNSW? (627)
MAG-3	ROKNSW^ (628)
EST66	CCPSSKEDSLNCIETMATTATCMKSNKGIEYSYAGGYCGKKKESCFG DKKPVTDYQQQTRNIPNPGGAAL^ (629)
G12.2	DESKCDRCNCAELRSSRCTQAIFCLTPELCTPSISCPTEGECRTKPH QSRCTRFVEQVFNKCRDA^ (630)
G12.1	DDSYCDGCLCTILKKTKTSTMSCRGT- CRKEWPCEBEDCYCTRIQG GACVTPSECKPGEC^ (631)
EST171	GCVYEGIEYSVGRTYQADCNTRCDGFDLATCTVAGCTGFGPE^ (632)
U010 homolog	SGPADCCRMKECCTDRVNECLQRYSGREDKFVSFCYQEATVTCGSFN EIVGCCYGYQCMIRVVKPNSLSGAHEACKTVSCGNPCA^ (633)
P29	DCCGVKLEMCHPCLCDNSCKNYGK# (634)
EST87	GEPIPTTVINYGECKDPSCWVKVDKFCPGASFPN^ (635)
Ge3.1 (F590)	QCCTFCNFGCQPCCVF^ (636)
Ts10.1	DGCPPHPVPGMHKCMCTNTC (637)
Conophysin-R	HPTKPCMYSFGQCQVGFHICCGPTGCEMGTAEANMCSEDEDFIPCVQ FGSDCALNNFDNIHGHCVDGLCCGVDDTCTTHLGCL^ (638)

\* Conopeptides grouped together are homologous.

[0080] It will be appreciated that the methods and compositions of the instant invention can be incorporated in the form of a variety of embodiments, only a few of which are disclosed herein. It will be apparent to the artisan that other embodiments exist and do not depart from the spirit of the invention. Thus, the described embodiments are illustrative and should not be construed as restrictive.

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